

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 60 Seconds
(without alignments)
56.510 Million cell updates/sec

Title: US-09-660-302D-2
Perfect score: 65
Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseq1980s.*
2: geneseq1990s.*
3: geneseq2000s.*
4: geneseq2001s.*
5: geneseq2002s.*
6: geneseq2003as.*
7: geneseq2003bs.*
8: geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	12	2 AAY32789	Aay32789 Growth ho
2	65	100.0	130	2 AAY32792	Aay32792 Growth ho
3	65	100.0	637	1 AAP92108	Aap92108 Human gro
4	65	100.0	638	1 AAP81326	Aap81326 Human gro
5	65	100.0	638	1 AAP81327	Aap81327 Rabbit gr
6	65	100.0	638	1 AAP92107	Aap92107 Rabbit gr
7	65	100.0	638	2 AAW33394	Aaw33394 Human gro
8	65	100.0	638	2 AAW33395	Aaw33395 Rabbit gr
9	65	100.0	638	7 ADD45061	Add45061 Rat Prote
10	65	100.0	638	7 ADD45067	Add45067 Human Pro
11	65	100.0	638	7 ADD45063	Add45063 Human Pro
12	65	100.0	638	7 ADD45065	Add45065 Rat Prote
13	65	100.0	648	4 ABB11437	Abb11437 Human gro
14	61	93.8	638	2 AAR06473	Aar06473 Serum som
15	59	90.8	12	2 AAY32794	Aay32794 Chicken G
16	59	90.8	608	2 AAR25246	Aar25246 Chicken G
17	53	81.5	12	2 AAY32793	Aay32793 Growth ho
18	48	73.8	1399	6 ABU41685	Abu41685 Protein e
19	48	73.8	1409	6 ABU29830	Abu29830 Protein e
20	45	69.2	705	5 ABB77350	Abb77350 Plodia in
21	40	61.5	193	3 AAG60096	Aag60096 Arabidops
22	40	61.5	203	3 AAG60095	Aag60095 Arabidops
23	40	61.5	251	6 ABM69113	Abm69113 Photorhab
24	40	61.5	1363	4 AAB37607	Aab37607 Human pro
25	40	61.5	1363	6 ABU04285	Abu04285 Human exp

26	39.5	60.8	300	5	ABB48962	Abb48962 Listeria
27	39	60.0	14	6	ADA09064	Ada09064 Lanthanid
28	39	60.0	163	3	AAW20448	Aaw20448 H. pylori
29	39	60.0	255	3	AAB53166	Aab53166 Macaca mu
30	39	60.0	321	2	AAW20847	Aaw20847 H. pylori
31	39	60.0	404	4	ABB58263	Abb58263 Drosophil
32	39	60.0	506	7	ADC97612	Adc97612 E. faeciu
33	39	60.0	939	6	ABM70226	Abm70226 Photorhab
34	39	60.0	1023	4	ABB70491	Abb70491 Drosophil
35	39	60.0	1399	4	AAU33683	Aau33683 Pseudomon
36	39	60.0	1399	6	ABU15652	Abu15652 Protein e
37	38	58.5	103	3	AAG43966	Aag43966 Zea mays
38	38	58.5	103	3	AAG40846	Aag40846 Zea mays
39	38	58.5	133	3	AAG43965	Aag43965 Zea mays
40	38	58.5	855	5	ABP66339	Abp66339 Bifidobac
41	38	58.5	2113	7	ADC00980	Adc00980 Enterohae
42	38	58.5	3460	5	ABB05007	Abb05007 Human ree
43	38	58.5	3460	7	ADE60143	Ade60143 Human pro
44	38	58.5	3461	5	ABB05008	Abb05008 Mouse ree
45	38	58.5	3461	5	ABB57065	Abb57065 Mouse isc

ALIGNMENTS

RESULT 1

AAV32789
ID AAY32789 standard; peptide; 12 AA.
XX
AC AAY32789;
XX
DT 09-NOV-1999 (first entry)
XX
DE Growth hormone receptor polypeptide for inhibition of receptor cleavage.
XX
DE Growth hormone receptor; signal transduction; proteolytic cleavage;
KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;
KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS.
XX
OS Mammalia.
XX
PN EP943624-A1.
XX
PD 22-SEP-1999.
XX
PF 12-MAR-1998; 98EP-00200799.
XX
PR 12-MAR-1998; 98EP-00200799.
XX
(UYUT-) RIJKSUNIV UTRECHT.
XX
WPI; 1999-510568/43.
XX
Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.
XX
Claim 11; Page 27; 36pp; English.

This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to any hormones which might be present. The binding sensitivity of cells to this sequence is an example, is located at or around a motif, of which this sequence is a complex binding site. The inhibitor ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

CC stress and during neuromuscular disease

SQ Sequence 12 AA;

Query Match 100.0%; Score 65; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
|||||

Db 1 DDSWVEFIELDI 12

RESULT 2

AY32792

ID AAY32792 standard; peptide; 130 AA.

XX AC AAY32792;

DT 09-NOV-1999 (first entry)

XX Growth hormone receptor polypeptide.

XX Signal transduction; proteolytic cleavage; growth hormone receptor;
KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;
KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
KW growth hormone deficiency.

XX OS Mammalia.

XX EP943624-A1.

PN 22-SEP-1999.

XX 12-MAR-1998; 98EP-00200799.

XX 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

CC Controlling the availability and/or signal transduction capability of a
CC cell surface receptor, useful for treating growth hormone deficiencies.
PS Disclosure; Page 5; 36pp; English.

CC This sequence is a growth hormone receptor polypeptide. Polypeptides for
CC the upregulation of the growth hormone receptor are derived from this
CC sequence e.g. AAY32793. Variants (AAY32794-Y32823) of the derived
CC ubiquitin/proteosome binding site located on the intracellular part of a
CC cell surface receptor. These sequences are used in a method for
CC controlling the availability and signal transduction capability of a cell
CC surface receptor by administering an inhibitor that is capable of
CC inhibiting proteolytic cleavage of the receptor. Inhibition of this
CC proteolytic cleavage results in the receptors being present on the
CC surface for longer and therefore signalling for longer to the interior of
CC the cell. This increases the sensitivity of cells to any hormones which
CC might be present. The inhibitor is either derived from, competes with or
CC binds to a polypeptide sequence of which sequences AAY32794-Y32823 are
CC examples. The inhibitor may be used to treat muscle wasting, associated
CC with disorders such as renal tubular defects, uraemia, diabetes,
CC Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and
CC during neuromuscular disease
XX Sequence 130 AA;

Query Match 100.0%; Score 65; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

Db 52 DDSWVEFIELDI 63

RESULT 3

AAP92108

ID AAP92108 standard; protein; 637 AA.

XX AC AAP92108;

DT 14-FEB-1990 (first entry)

XX Human growth hormone receptor.

DE Growth hormone receptor.

KW Growth hormone receptor.

OS Homo sapiens.

PN US4857637-A.

PD 15-AUG-1989.

XX 12-JUN-1987; 87US-00061942.

XX 22-MAY-1985; 85US-00737302.

XX 07-MAY-1986; 86US-00861236.

XX (GETH) GENENTECH INC.

PI Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;

DR WPI; 1989-300419/41.

XX N-PSDB; AAN91325.

PT Modulating growth hormone receptor activity - by immunising animal
PT against growth hormone receptor extracellular domain deriv. to raise
PT antiserum.

PS Disclosure; Fig 2a-c; 18pp; English.

XX An animal can be immunised against its growth hormone receptor by
CC vaccinating against a growth hormone receptor extracellular domain deriv.
CC predetermined to raise polyclonal antisera which affect the receptor as a
CC growth hormone agonist. This method enables continuous growth of target
CC tissues without frequent hormone admin
XX Sequence 637 AA;

QY 1 DDSWVEFIELDI 12

Db 339 DDSWVEFIELDI 350

Query Match 100.0%; Score 65; DB 1; Length 637;

Best Local Similarity 100.0%; Pred. No. 0.031;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

Db 339 DDSWVEFIELDI 350

RESULT 4

AAP81326

ID AAP81326 standard; protein; 638 AA.

XX AC AAP81326;

DT 23-OCT-1990 (first entry)

XX Human growth hormone receptor.

DE Growth hormone receptor; gigantism; acromegaly.

KW Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1.18

```

FT XX /label= signal_sequence
FN PN WO8809818-A.
XX XX
XX PD 15-DEC-1988.
XX XX
XX PF 10-JUN-1988; 88WO-US002008.
XX XX
XX PR 12-JUN-1987; 87US-00062542.
XX XX
XX PA (GETH ) GENENTECH INC.
XX XX
XX PI Hammonds RG, Leung D, Wood WI;
XX XX
XX DR WPI; 1988-368632/51.
XX DR N-PSDB; AAN81716.
XX XX
XX PT New pure growth hormone receptor and binding protein - for treating
XX PT growth hormone abnormalities, and new encoding DNA sequences.
XX PS Disclosure; Page ?; lpp; English.
XX CC
XX CC The sequence was deduced from a clone isolated from an adult liver cDNA
XX CC lambda gt10 library. The DNA can be inserted into an expression vector
XX CC for prodn. of the recombinant GHR which is used to treat GH-related
XX CC disorders such as gigantism and acromegaly. A hydropathy plot revealed an
XX CC extracellular GH binding domain, a transmembrane domain, and an
XX CC intracellular signalling domain. Eight potential N-linked glycosylation
XX CC sites are predicted. See also AAP81327 and AAN81718-9
XX XX
XX SQ Sequence 638 AA;

Query Match 100.0%; Score 65; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 339 DDSWVEFIELDI 350

RESULT 6
AAP92107
ID AAP92107 standard; protein; 638 AA.
XX AAP92107;
XX DT 13-FEB-1990 (first entry)
XX DE Rabbit growth hormone receptor.
XX KW Growth hormone receptor; rabbit.
XX OS Oryctolagus cuniculus.
XX PN US4857637-A.
XX PD 15-AUG-1989.
XX PF 12-JUN-1987; 87US-00061942.
XX PR 22-MAY-1985; 85US-00737302.
XX PR 07-MAY-1986; 86US-00861236.
XX PA (GETH ) GENENTECH INC.
XX PI Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;
XX XX
XX DR WPI; 1989-300419/41.
XX DR N-PSDB; AAN91323.
XX XX
XX PT Modulating growth hormone receptor activity - by immunising animal
XX PT against growth hormone receptor extracellular domain deriv. to raise
XX PT antisera.
XX PS Disclosure; Fig 1a-c; 18pp; English.
XX XX
XX CC An animal can be immunised against its growth hormone receptor by
XX CC vaccinating against a growth hormone receptor extracellular domain deriv.
XX CC predetermined to raise polyclonal antisera which affect the receptor as a
XX CC growth hormone agonist. This method enables continuous growth of target
XX CC tissues without frequent hormone admin
XX XX
XX SQ Sequence 638 AA;

Query Match 100.0%; Score 65; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 339 DDSWVEFIELDI 350

RESULT 5
AAP81327
ID AAP81327 standard; protein; 638 AA.
XX AAP81327;
XX DT 23-OCT-1990 (first entry)
XX DE Rabbit growth hormone receptor.
XX KW Growth hormone receptor; rabbit; gigantism; acromegaly.
XX OS Oryctolagus cuniculus.
XX PN WO8809818-A.
XX PD 15-DEC-1988.
XX PF 10-JUN-1988; 88WO-US002008.
XX PR 12-JUN-1987; 87US-00062542.
XX PA (GETH ) GENENTECH INC.
XX PI Hammonds RG, Leung D, Wood WI;
XX DR WPI; 1988-368632/51.
XX DR N-PSDB; AAN81717.

```

```

QY      1 DDSWVEFIELDI 12
Db      339 DDSWVEFIELDI 350

RESULT 7
AAW33394
XX      AAW33394 standard; protein; 638 AA.
AC      AAW33394;
XX      25-MAR-2003 (revised)
DT      11-MAY-1998 (first entry)
XX      Human growth hormone receptor.
DE      Growth hormone receptor; growth hormone binding protein; somatotropin;
KW      human; gigantism; acromegaly; therapy.
XX      Homo sapiens.
OS      Key      Location/Qualifiers
FH      Peptide      1..18
FT      /label= sig_peptide
FT      Domain      247..269
FT      /note= "transmembrane domain"
FT      Misc-difference 375
FT      /note= "translated codon is Ser in clone ghr.210 and
FT      ghr.110, Ile in ghr.501"
XX      US5688763-A.
XX      18-NOV-1997.
XX      25-MAY-1994; 94US-00248832.
XX      12-JUN-1987; 87US-00062542.
XX      28-JUN-1991; 91US-00723358.
XX      08-JAN-1993; 93US-00002489.
XX      (LEUN/) LEUNG D W.
XX      (HAMM/) HAMMONDS R G.
XX      (WOOD/) WOOD W I.
XX      (COLO/) COLOSI P C.
XX      (SPEN/) SPENCER S A.
XX      Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;
XX      WPI; 1998-008010/01.
XX      N-PSDB; AAT94063.
XX      Human and rabbit growth hormone receptor protein - useful to treat
XX      disorders associated with overexpression, e.g. gigantism and acromegaly.
XX      Claim 2; Fig 8a; 60pp; English.
XX      This protein sequence comprises human growth hormone receptor. The amino
XX      acid sequence was deduced from cDNA clones (see AAT94063) obtained from a
XX      human liver cDNA library, and shows 84% identity to the rabbit growth
XX      hormone receptor (see AAW33395). Human growth hormone receptor, its
XX      derivatives in which the cytoplasmic or transmembrane domains are
XX      deleted, and growth hormone binding proteins comprising amino acids 190-
XX      246 or 1-324 of the mature protein, can be used to treat disorders
XX      associated with growth hormone over-expression, e.g. gigantism and
XX      acromegaly. The binding protein may also be used to increase the
XX      stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
XX      to correct PF field.)
XX      SQ      Sequence 638 AA;
Query Match      100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 DDSWVEFIELDI 12
Db      339 DDSWVEFIELDI 350

RESULT 8
AAW33395
XX      AAW33395 standard; protein; 638 AA.
AC      AAW33395;
XX      25-MAR-2003 (revised)
DT      11-MAY-1998 (first entry)
XX      Rabbit growth hormone receptor.
DE      Growth hormone receptor; growth hormone binding protein; somatotropin;
KW      rabbit; gigantism; acromegaly; therapy.
XX      Oryctolagus cuniculus.
OS      Key      Location/Qualifiers
FH      Peptide      1..18
FT      /label= Sig_peptide
FT      Misc-difference 49
FT      /note= "translated codon is Ala in clone ghr.435, Thr in
FT      ghr.440"
FT      Domain      247..269
FT      /note= "transmembrane domain"
XX      US5688763-A.
XX      18-NOV-1997.
XX      25-MAY-1994; 94US-00248832.
XX      12-JUN-1987; 87US-00062542.
XX      28-JUN-1991; 91US-00723358.
XX      08-JAN-1993; 93US-00002489.
XX      (LEUN/) LEUNG D W.
XX      (HAMM/) HAMMONDS R G.
XX      (WOOD/) WOOD W I.
XX      (COLO/) COLOSI P C.
XX      (SPEN/) SPENCER S A.
XX      Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;
XX      WPI; 1998-008010/01.
XX      N-PSDB; AAT94064.
XX      Human and rabbit growth hormone receptor protein - useful to treat
XX      disorders associated with overexpression, e.g. gigantism and acromegaly.
XX      Claim 2; Fig 8b; 60pp; English.
XX      This protein sequence comprises rabbit growth hormone receptor. The amino
XX      acid sequence was deduced from cDNA clones (see AAT94064) obtained from a
XX      rabbit liver cDNA library, and shows 84% identity to the human growth
XX      hormone receptor (see AAW33394). Rabbit and human growth hormone
XX      receptors, their derivatives in which the cytoplasmic or transmembrane
XX      domains are deleted, and growth hormone binding proteins comprising amino
XX      acids 190-246 or 1-324 of the mature proteins, can be used to treat
XX      disorders associated with growth hormone over-expression, e.g. gigantism
XX      and acromegaly. The binding protein may also be used to increase the
XX      stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
XX      to correct PF field.)
XX      SQ      Sequence 638 AA;
Query Match      100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;

```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | |
Db 339 DDSWVEFIELDI 350

RESULT 9
ADD45061
ID ADD45061 standard; protein; 638 AA.
XX AC ADD45061;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein P16310, SEQ ID NO 10493.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P16310.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a rat protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 638 AA;
Query Match 100.0%; Score 65; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031; 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | |
Db 340 DDSWVEFIELDI 351

RESULT 10
ADD45067
ID ADD45067 standard; protein; 638 AA.
XX AC ADD45067;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein P10912, SEQ ID NO 10499.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P10912.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
derivative or allelic variation of the nucleic acid sequence. Also
claimed are a vector comprising the novel polynucleotide, a host cell
comprising the vector, a method for identifying a nucleotide sequence
which is differentially regulated in an animal subjected to pain and a
kit to perform the method, an array, a method for identifying an agent
that increases or decreases the expression of the polynucleotide sequence
that is differentially expressed in neuronal tissue of a first animal
subjected to pain, a method for identifying a compound which regulates
the expression of a polynucleotide sequence which is differentially
expressed in an animal subjected to pain, a method for identifying a
compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 638 AA;

Query Match 100.0%; Score 65; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIEDI 12
| | | | | | | | | |
Db 339 DDSWVEFIEDI 350

RESULT 11

ADD45063
ID ADD45063 standard; protein; 638 AA.

XX AC ADD45063;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P10912, SEQ ID NO 10495.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX PR WPI; 2003-268312/26.

XX PR GENBANK; P10912.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 65; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIEDI 12
| | | | | | | | | |
Db 339 DDSWVEFIEDI 350

RESULT 12

ADD45065
ID ADD45065 standard; protein; 638 AA.

XX AC ADD45065;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P16310, SEQ ID NO 10497.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX PR WPI; 2003-268312/26.

XX PR GENBANK; P16310.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 638 AA;
 CC
 CC Query Match 100.0%; Score 65; DB 7; Length 638;
 CC Best Local Similarity 100.0%; Pred. No. 0.031;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DDSWVEFIELDI 12
 CC |||||
 CC Db 340 DDSWVEFIELDI 351
 CC
 CC RESULT 13
 CC ID ABB11437 standard; peptide; 648 AA.
 CC AC ABB11437;
 CC DT 11-JAN-2002 (first entry)
 CC XX
 CC DE Human growth hormone receptor homologue, SEQ ID NO:1807.
 CC
 CC KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 CC KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 CC KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 CC KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 CC KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 CC KW chronic inflammatory condition; proliferative retinopathy;
 CC KW atherosclerosis; coronary heart disease; arterial ischaemia;
 CC KW bone disorder; osteoporosis; vascular growth disorder;
 CC KW tissue regeneration; wound healing; infection; immune disorder;
 CC KW cell culture; drug screening; gene therapy; antiinflammatory;
 CC KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 CC KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 CC KW antifungal; vulnery; antiulcer.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC PN WO200157188-A2.
 CC XX
 CC PD 09-AUG-2001.
 CC XX
 CC PF 05-FEB-2001; 2001WO-US003800.
 CC XX
 CC PR 03-FEB-2000; 2000US-00496914.
 CC PR 27-APR-2000; 2000US-00560875.
 CC XX
 CC PA (HYSE-) HYSEQ INC.
 CC XX
 CC PI Tang YT, Liu C, Drmanac RT;
 CC XX
 CC DR WPI; 2001-457740/49.
 CC DR N-PSDB; ABA08681.
 CC XX
 CC PT Human proteins and DNA encoding sequences useful for preventing, treating
 CC PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 CC PT and cancer.
 CC XX
 CC PS Claim 20; Page 189-190; 1963pp; English.
 CC XX

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides,
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth factor activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 CC
 CC Sequence 648 AA;
 CC
 CC Query Match 100.0%; Score 65; DB 4; Length 648;
 CC Best Local Similarity 100.0%; Pred. No. 0.031;
 CC Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 DDSWVEFIELDI 12
 CC |||||
 CC Db 349 DDSWVEFIELDI 360
 CC
 CC RESULT 14
 CC AAR06473
 CC ID AAR06473 standard; protein; 638 AA.
 CC AC AAR06473;
 CC XX
 CC DT 27-AUG-2003 (revised)
 CC DT 04-JAN-1991 (first entry)
 CC XX
 CC DE Serum somatotropin receptor protein from clone PRAT7-12.
 CC XX
 CC KW Somatotropin receptor; SR; somatotropin binding protein; SBP; PRAT7-12;
 CC KW PRAT1-6.
 CC XX
 CC OS Rattus rattus.
 CC XX
 CC FH Key Location/Qualifiers
 CC FT Peptide 1..17
 CC FT /label= signal_sequence
 CC FT 262..638
 CC FT Region /label= divergence
 CC FT /note= "non-homology region with SBP/pRTAI-6"
 CC FT 264..289
 CC FT Domain /label= transmembrane_domain

XX EP383205-A.
 XX 22-AUG-1990.
 XX 09-FEB-1990; 90EP-00102552.
 XX 17-FEB-1989; 89US-00310725.
 XX (AMCY) AMERICAN CYANAMID CO.
 PA Logan JS, Baumbach WR;
 PI WPI; 1990-255493/34.
 XX N-PSDB; AAQ05691.
 XX
 PT Somatotropin binding protein and gene - used to regulate and/or modify
 PT activity of somatotropin in humans and animals.
 XX Disclosure; Fig 6; 43pp; English.
 XX Homology comparison between this putative rat somatotropin receptor and
 CC the published sequence indicates 70% identity. See also AAQ05689-91,
 CC AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 638 AA;
 Query Match 93.8%; Score 61; DB 2; Length 638;
 Best Local Similarity 91.7%; Pred. No. 0.14;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DDSWVEFIELDI 12
 DQ :|||||||
 DB 340 DESWVEFIELDI 351
 RESULT 15
 AAY32794
 ID AAY32794 standard; peptide; 12 AA.
 XX
 AC AAY32794;
 XX
 DT 09-NOV-1999 (first entry)
 XX
 DE Chicken growth hormone receptor derived polypeptide.
 XX
 KW Signal transduction; proteolytic cleavage; growth hormone receptor;
 KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;
 KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
 KW growth hormone deficiency; inhibitor.
 XX
 OS Gallus gallus.
 XX
 XX EP943624-A1.
 XX
 PD 22-SEP-1999.
 XX
 PF 12-MAR-1998; 98EP-00200799.
 XX
 PR 12-MAR-1998; 98EP-00200799.
 XX
 XX (UYUT-) RIJKSUNIV UTRECHT.
 PA
 XX WPI; 1999-510568/43.
 DR
 XX Controlling the availability and/or signal transduction capability of a
 PT cell surface receptor, useful for treating growth hormone deficiencies.
 PT
 XX Disclosure; Page 9; 36pp; English.
 PS
 XX This sequence is a polypeptide from the chicken growth hormone receptor.
 CC Sequences (AAY32794-Y32823) are examples of polypeptide sequences found
 CC at or near the ubiquitin/proteosome complex binding site located on the

CC intracellular part of a cell surface receptor. These sequences are used
 CC in a method for controlling the availability and signal transduction
 CC capability of a cell surface receptor by administering an inhibitor that
 CC is capable of inhibiting proteolytic cleavage of the receptor. Inhibition
 CC of this proteolytic cleavage results in the receptors being present on
 CC the surface for longer and therefore signalling for longer to the
 CC interior of the cell. This increases the sensitivity of cells to any
 CC hormones which might be present. The inhibitor is either derived from,
 CC competes with or binds to a polypeptide sequence of which sequences
 CC AAY32794-Y32823 are examples. The inhibitor may be used to treat muscle
 CC wasting, associated with disorders such as renal tubular defects,
 CC uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS,
 CC after stress and during neuromuscular disease
 XX
 SQ Sequence 12 AA;
 Query Match 90.8%; Score 59; DB 2; Length 12;
 Best Local Similarity 91.7%; Pred. No. 0.0041;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DDSWVEFIELDI 12
 DQ :|||||||
 DB 1 DDLWVEFIELDI 12

Search completed: June 9, 2004, 15:48:26
 Job time : 62 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 13.2973 Seconds
(without alignments)
86.807 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	100.0	634	2 S33339	somatotropin recep
2	65	100.0	638	2 A33505	somatotropin recep
3	65	100.0	638	2 A33991	somatotropin recep
4	65	100.0	638	2 B28176	somatotropin recep
5	65	100.0	638	2 S12136	somatotropin recep
6	65	100.0	677	2 S33608	somatotropin-bind
7	59	90.8	608	2 S32823	somatotropin recep
8	48	73.8	702	2 A61619	arylphorin precurs
9	43	66.2	411	2 S66916	hypothetical prote
10	43	66.2	704	2 A34287	storage protein 2
11	41	63.1	1379	2 JC4954	vascular endotheli
12	40	61.5	442	2 AD2113	hypothetical prote
13	40	61.5	1363	2 I58375	protein-tyrosine k
14	39.5	60.8	300	2 AF1115	transcription regu
15	39.5	60.8	300	2 AG1476	signal recognition
16	39	60.0	103	2 T03951	hypothetical prote
17	39	60.0	217	2 AG2426	probable 3-oxoacyl
18	39	60.0	264	1 E70027	hypothetical prote
19	39	60.0	321	2 H71924	hypothetical prote
20	39	60.0	321	2 B64589	hypothetical prote
21	39	60.0	829	2 T19514	hypothetical prote
22	39	60.0	1399	2 G83112	DNA-directed RNA p
23	38	58.5	363	2 S75238	hypothetical prote
24	38	58.5	489	2 T27468	hypothetical prote
25	38	58.5	698	1 S00742	cytochrome-c oxida
26	38	58.5	2113	2 G91286	probable RNA helic
27	38	58.5	2113	2 C86128	probable helicase
28	38	58.5	3461	2 S58870	reelin precursor -
29	37.5	57.7	3707	2 S18252	heparan sulfate pr

30	37.5	57.7	4391	2 A38096	perlecan precursor
31	37	56.9	190	2 AI3299	5-methylcytosine-s
32	37	56.9	198	2 E70357	conserved hypothet
33	37	56.9	258	2 S74631	hypothetical prote
34	37	56.9	339	1 NCBPX4	exonuclease 47 (EC
35	37	56.9	436	2 D64028	hypothetical prote
36	37	56.9	457	2 G69341	conserved hypothet
37	37	56.9	473	2 C96516	FL6N3.15 [imported
38	37	56.9	595	2 AF2097	hypothetical prote
39	37	56.9	648	2 T09036	hypothetical prote
40	37	56.9	804	2 A39972	segment S5 protein
41	37	56.9	840	2 T36175	probable large ATP
42	37	56.9	1263	2 T13805	spalt-related prot
43	37	56.9	1298	2 A48999	protein-tyrosine k
44	36.5	56.2	355	2 S18510	MATa1 splicing fac
45	36.5	56.2	1107	2 S61667	probable membrane

ALIGNMENTS

RESULT 1

S33339

somatotropin receptor - sheep

N;Alternate names: growth hormone receptor

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 02-Aug-2002

C;Accession: S33339

R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.

Mol. Cell. Endocrinol. 73, 135-145, 1990

A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expr

A;Reference number: S33339; MUID:91099608; PMID:1980117

A;Accession: S33339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-634 <ADA>

A;Cross-references: EMBL:M82912; NID:g165888; PIDN:AAA73171.1; PID:g165889

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

Query Match 100.0%; Score 65; DB 2; Length 634;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12

|||||

Db 335 DDSWVEFIELDI 346

RESULT 2

A33505

somatotropin receptor precursor - rat

N;Alternate names: growth hormone receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 02-Aug-2002

C;Accession: A32985; A33505

R;Baumbach, W.R.; Horner, D.L.; Logan, J.S.

Genes Dev. 3, 1199-1205, 1989

A;Title: The growth hormone-binding protein in rat serum is an alternatively spliced for

A;Reference number: A32985; MUID:9006741; PMID:2792761

A;Accession: A32985

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <BAU>

A;Cross-references: GB:X16726

R;Mathews, L.S.; Enberg, B.; Norstedt, G.

J. Biol. Chem. 264, 9905-9910, 1989

A;Title: Regulation of rat growth hormone receptor gene expression.

A;Reference number: A33505; MUID:89255563; PMID:2722883

A;Accession: A33505

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <MAT>

A;Cross-references: GB:J04811; NID:g204308; PIDN:AAA41219.1; PID:g204309

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein

Query Match 100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | | | |
Db 340 DDSWVEFIELDI 351

RESULT 3

A33991
somatotropin receptor precursor - human
N;Alternate names: growth hormone receptor
N;Contains: somatotropin-binding protein, serum
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 02-Aug-2002
C;Accession: A33991; S04530
R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R
Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989
A;Title: Characterization of the human growth hormone receptor gene and demonstration of
A;Reference number: A33991; MUID:90046742; PMID:2813379
A;Accession: A33991
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-638 <GOD>
A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;
Nature 330, 537-543, 1987
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex
A;Reference number: S04530; MUID:88065896; PMID:2825030
A;Accession: S04530

A;Molecule type: mRNA

A;Residues: 1-543, '1', '545-638 <LEU>
A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738
C;Genetics:
A;Gene: GDB:GHR
A;Cross-references: GDB:l11984; OMIM:600946
A;Map position: Spl3-Spl2
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: liver; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-638/Product: somatotropin receptor #status predicted <MAT>
F;265-288/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | | | |
Db 339 DDSWVEFIELDI 350

RESULT 4

B28176
somatotropin receptor precursor, hepatic - rabbit
N;Alternate names: growth hormone receptor
N;Contains: somatotropin-binding protein, serum
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1990 #sequence_revision 10-Mar-1994 #text_change 02-Aug-2002
C;Accession: S08544; A28176
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;
Nature 330, 537-543, 1987
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex
A;Reference number: S04530; MUID:88065896; PMID:2825030
A;Accession: S08544
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-638 <LEU>
A;Cross-references: GB:AF015252; NID:g2342651; PIDN:AA67613.1; PID:g2342652

A;Note: part of this sequence, including the amino end of the mature protein, was confi
R;Spencer, S.A.; Hammonds, R.G.; Henzel, W.J.; Rodriguez, H.; Waters, M.J.; Wood, W.I.
J. Biol. Chem. 263, 7862-7867, 1988

A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification,
A;Reference number: A92721; MUID:88227992; PMID:3372509

A;Accession: B28176

A;Molecule type: protein

A;Residues: 19-34; 'SPG', 81-88; 'X', 99, 'XX', 102-105, 'X', 107-110, 'XX', 113-114, 'X', 141, 'X',
-574, 'X', 576-577; 579-595 <SPE>

A;Note: sequence is derived from intact receptor

A;Accession: A28176

A;Molecule type: protein

A;Residues: 'XXX', 22-45, 'X', 47-55 <SP2>

A;Note: sequence is derived from a soluble form of the receptor isolated from serum
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status experimental <MAT>

F;265-288/Domain: transmembrane #status predicted <TMM>

F;46,200/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | | | |
Db 339 DDSWVEFIELDI 350

RESULT 5

S12136
somatotropin receptor precursor - pig
N;Alternate names: growth hormone receptor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S12136
R;Cioffi, J.A.; Wang, X.; Kopchick, J.J.
Nucleic Acids Res. 18, 6451, 1990
A;Title: Porcine growth hormone receptor cDNA sequence.
A;Reference number: S12136; MUID:91057155; PMID:2243805
A;Accession: S12136
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-638 <CIO>
A;Cross-references: EMBL:X54429; NID:g2037; PIDN:CAA38301.1; PID:g2038
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein

Query Match 100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | | | | | | | | | |
Db 339 DDSWVEFIELDI 350

RESULT 6

S33608
somatotropin-binding protein, high molecular weight, precursor - mouse
N;Alternate names: growth hormone-binding protein, high molecular weight
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Aug-2002
C;Accession: S33608; S33607
R;Smith, W.C.; Kuniyoshi, J.; Talamantes, F.
Mol. Endocrinol. 3, 984-990, 1989
A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular
A;Reference number: S33607; MUID:89295449; PMID:2739661
A;Accession: S33608
A;Molecule type: mRNA
A;Residues: 1-677 <SMI>
A;Cross-references: EMBL:M33324; NID:g193508; PIDN:AAA37690.1; PID:g309253

A;Experimental source: liver

A;Accession: S33607

A;Molecule type: mRNA

A;Residues: 1-324 <SM2>

A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; receptor; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-677/Product: somatotropin-binding protein, high molecular weight #status predicted

F;274-297/Domain: transmembrane #status predicted <TM>

F;40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 65; DB 2; Length 677;

Best Local Similarity 100.0%; Pred. No. 0.0039;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 375 DDSWVEFIELDI 386

RESULT 7

S32823

somatotropin receptor precursor, major splice form - chicken

N;Alternate names: growth hormone receptor

N;Contains: somatotropin receptor, short form

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Aug-2002

C;Accession: S32823; A49812

R;Burnside, J.; Liou, S.S.; Cogburn, L.A.

Endocrinology 128, 3183-3192, 1991

A;Title: Molecular cloning of the chicken growth hormone receptor complementary deoxyrib

A;Reference number: S32823; MUID:91243665; PMID:2036984

A;Accession: S32823

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-608 <BUR>

A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811

R;Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.

Mol. Endocrinol. 7, 1391-1398, 1993

A;Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf c

A;Reference number: A49812; MUID:94158898; PMID:8114754

A;Accession: A49812

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <HUA>

A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138

A;Experimental source: liver, normal chicken

A;Note: this truncated form is a minor splice form in normal chickens and the major form

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane protei

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-109/Product: somatotropin receptor, short form #status predicted <SHO>

Query Match 90.8%; Score 59; DB 2; Length 608;

Best Local Similarity 91.7%; Pred. No. 0.036;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 312 DDWVEFIELDI 323

RESULT 8

A61619

arylphorin precursor - greater wax moth

N;Alternate names: phenylalanine-rich protein lhp76

C;Species: Galleria mellonella (greater wax moth)

C;Date: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999

C;Accession: A61619

R;Mammel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.

Insect Biochem. Mol. Biol. 22, 333-342, 1992

A;Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellonella

A;Reference number: A61619

A;Accession: A61619

A;Molecule type: DNA

A;Residues: 1-702 <MEM>

A;Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078

A;Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dupl

C;Genetics:

A;Introns: 30/1; 74/3; 352/3; 410/2

A;Note: single copy gene

C;Superfamily: arylphorin

C;Keywords: glycoprotein; hemolymph; storage protein

F;1-16/Domain: signal sequence #status predicted <SIG>

F;211,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.8%; Score 48; DB 2; Length 702;

Best Local Similarity 63.6%; Pred. No. 3.1;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELD 11

|||||

Db 546 EDWINFIELD 556

RESULT 9

S66916

hypothetical protein YOR042w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein O2762

C;Species: Saccharomyces cerevisiae

C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C;Accession: S66916

R;Landt, O.; Hiesel, R.; Unseld, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66907

A;Accession: S66916

A;Molecule type: DNA

A;Residues: 1-411 <LAN>

A;Cross-references: EMBL:Z74949; NID:g1420165; PID:e251966; PID:g1420167; GSPDB:GN00015

A;Experimental source: strain S288C

C;Genetics:

A;Gene: MIPS:YOR042w

A;Cross-references: SGD:S0005568

A;Map position: 15R

Query Match 66.2%; Score 43; DB 2; Length 411;

Best Local Similarity 50.0%; Pred. No. 12;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 223 EDSWSQFVEKDL 234

RESULT 10

A34287

storage protein 2 - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 04-Sep-1998

C;Accession: A34287

R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.

J. Biol. Chem. 264, 11020-11025, 1989

A;Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mori

A;Reference number: A34287; MUID:89291839; PMID:2544581

A;Accession: A34287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-704 <FUJ>

C;Superfamily: arylphorin

Query Match 66.2%; Score 43; DB 2; Length 704;

Best Local Similarity 54.5%; Pred. No. 22;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVERFIELD 11
:|:|:|
Db 543 EDNWKFFELD 553

RESULT 11

JC4954
vascular endothelial growth factor receptor 2 precursor - Japanese quail
N;Alternate names: Quail endothelial kinase 2; Quek 2
C;Species: Coturnix coturnix japonica (Japanese quail)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999
C;Accession: JC4954
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
Gene 174, 3-8, 1996

A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
A;Reference number: JC4953; MUID:97017121; PMID:8863722

A;Accession: JC4954
A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1379 <EIC>

A;Cross-references: EMBL:X83287; NID:q619865; PIDN:CAA58267.1; PID:e283815; PID:gl707416
C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;769-810/Domain: transmembrane #status predicted <TM>

F;856-1188/Domain: protein kinase homolog <KIN>

F;864-872/Region: protein kinase ATP-binding motif

Query Match 63.1%; Score 41; DB 2; Length 1379;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DSWVEFIE 9

Db 519 DTWVEFVE 526
|:|:|:|:|

RESULT 12

AD2113

hypothetical protein all2459 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C;Accession: AD2113

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AD2113

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-442 <KUR>

A;Cross-references: GB:BA000019; PIDN:BA874158.1; PID:gl7131551; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all2459

Query Match

Best Local Similarity 61.5%; Score 40; DB 2; Length 442;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIEL 10

||||:|:|

Db 225 DDSWYDIKL 234

RESULT 13

I58375

protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Feb-2000

C;Accession: I58375; B42010
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris,
Oncogene 8, 2293-2298, 1993
A;Title: Molecular cloning of murine FLT and FLT4.

A;Reference number: I58375; MUID:93330572; PMID:8393164

A;Accession: I58375

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1363 <RES>

A;Cross-references: GB:I07296; NID:g293780; PIDN:AAA40077.1; PID:g293781

R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.

Genomics 13, 475-478, 1992

A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.

A;Reference number: A42010; MUID:92307693; PMID:1319394

A;Accession: B42010

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: DNA

A;Residues: 1033-1072 <GAL>

C;Genetics:

A;Gene: FLT4

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

F;843-1176/Domain: protein kinase homolog <KIN>

F;851-859/Region: protein kinase ATP-binding motif

Query Match 61.5%; Score 40; DB 2; Length 1363;

Best Local Similarity 75.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSWVEFIE 9

||||:|:|

Db 505 DSWTEFVE 512

RESULT 14

AF1115

transcription regulators homolog lmo0325 [imported] - Listeria monocytogenes (strain EGD

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AF1115

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1115

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-300 <GLA>

A;Cross-references: GB:NC_003210; PIDN:CAD00852.1; PID:gl6409689; GSPDB:GN00177

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo0325

Query Match

Best Local Similarity 60.8%; Score 39.5; DB 2; Length 300;

Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 DDSWVEFIEL 10

||||:|:|

Db 73 DDSFWIDFVEL 83

RESULT 15

AG1476

transcription regulators homolog lmo0350 [imported] - Listeria innocua (strain Clip1126)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AG1476

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of *Listeria* species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1476
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-300 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC95583.1; PID:g16412779; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0350

Query Match 60.8%; Score 39.5; DB 2; Length 300;
Best Local Similarity 63.6%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 DDS-WVEFIEL 10
Db 73 DDSFWIDFVEL 83

Search completed: June 9, 2004, 15:52:16
Job time : 14.2973 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:55 ; Search time 8.75676 Seconds
(without alignments)
71.355 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	634	1	GHR_BOVIN
2	65	100.0	634	1	GHR_SHEEP
3	65	100.0	638	1	GHR_HUMAN
4	65	100.0	638	1	GHR_MACMU
5	65	100.0	638	1	GHR_PIG
6	65	100.0	638	1	GHR_RABIT
7	65	100.0	638	1	GHR_RAT
8	65	100.0	650	1	GHR_MOUSE
9	59	90.8	608	1	GHR_CHICK
10	59	90.8	611	1	GHR_COLLI
11	48	73.8	1409	1	RPOC_PSEPU
12	43	66.2	704	1	SSP2_BOMMO
13	40	61.5	358	1	Y4FP_RHISN
14	40	61.5	1363	1	VGR3_MOUSE
15	39	60.0	103	1	SR09_MAIZE
16	39	60.0	1399	1	RPOC_PSEAE
17	38	58.5	698	1	COX1_TETPY
18	38	58.5	3460	1	RELN_HUMAN
19	38	58.5	3461	1	RELN_MOUSE
20	38	58.5	3462	1	RELN_RAT
21	37.5	57.7	3707	1	PGBM_MOUSE
22	37.5	57.7	4391	1	PGBM_HUMAN
23	37	56.9	173	1	GLBC_NIPBR
24	37	56.9	339	1	EXOI_EPT4
25	37	56.9	341	1	MURB_SHECN
26	37	56.9	436	1	YEO9_HAEIN
27	37	56.9	804	1	VP5_WTV
28	37	56.9	1298	1	VGR3_HUMAN
29	36.5	56.2	355	1	AAR2_YEAST
30	36	55.4	209	1	COAT_TRVPS
31	36	55.4	243	1	YOEF_BACSU
32	36	55.4	260	1	THI4_ARCFU
33	36	55.4	316	1	YQ15_CABEL
					Q9278 caenorhabdi

34 36 55.4 447 1 HST3_YEAST
35 36 55.4 506 1 YF26_SYNY3
36 36 55.4 531 1 YQCG_BACSU
37 36 55.4 694 1 FRES_YEAST
38 36 55.4 724 1 CAO2_CANMA
39 36 55.4 897 1 BGAL_CLOAB
40 36 55.4 1094 1 YB00_YEAST
41 36 55.4 1355 1 SALM_DROME
42 36 55.4 1402 1 SALM_DROVI
43 35 53.8 126 1 YVQI_BACSU
44 35 53.8 263 1 THI4_METJA
45 35 53.8 306 1 LUXD_PHOPO

P53687 saccharomyc
P74360 synechoyst
P45942 bacillus su
Q08908 saccharomyc
Q00468 candida mal
P24131 clostridium
P38114 saccharomyc
P39770 drosophila
P39806 drosophila
Q32202 bacillus su
Q58018 methanococc
P41302 photobacter

ALIGNMENTS

RESULT 1
GHR_BOVIN
ID GHR_BOVIN STANDARD; PRT; 634 AA.
AC P79108,1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
DE Protein).
GN GHR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=GIR; TISSUE=Liver;
RA Souza S.C., Wang X., Lobo R.B., Kopchick J.J.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X70041; CAA49635.1; -.
CC HSSP; P10912; 1A22.
CC InterPro; IPR002996; CR1A.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR003528; Hemtopoptn_L_Fl.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L Fl; 1.
CC Receptor; Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 18
FT CHAIN 19 634
FT DOMAIN 19 260
FT TRANSMEM 261 284
FT DOMAIN 285 634
FT DOMAIN 141 248
FT DISULFID 56 66
FT DISULFID 97 108
FT DISULFID 122 136
FT CARBOHYD 46 46
FT CARBOHYD 73 73
FT CARBOHYD 111 111

```
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CBD2E CRC64;

Query Match 100.0%; Score 65; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | |
Db 335 DDSWVEFIELDI 346

RESULT 2
GHR_SHEEP
ID GHR_SHEEP STANDARD; PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver.";
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormones.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; M82912; AAA73171.1; -.
DR FIR; S33339; S33339.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 634
FT DOMAIN 19 260
FT TRANSMEM 261 284
FT DOMAIN 285 634
FT DOMAIN 141 248
FT DISULFID 56 66
FT DISULFID 97 108
FT DISULFID 122 136
FT CARBOHYD 46 46
FT CARBOHYD 73 73
N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; FFD28B9C23EC1496 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
| | | | | | | | | |
Db 335 DDSWVEFIELDI 346

RESULT 3
GHR_HUMAN
ID GHR_HUMAN STANDARD; PRT; 638 AA.
AC P10312;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=88065896; PubMed=2825030;
RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,
RA Henzel W.J., Barnard R., Waters M.J., Wood W.I.;
RT "Growth hormone receptor and serum binding protein: purification,
RT cloning and expression.";
RL Nature 330:537-543(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LEU-544.
RX MEDLINE=90046742; PubMed=2813379;
RA Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,
RA Keret R., Rotwein P.S., Parks J.S., Laron Z., Wood W.I.;
RT "Characterization of the human growth hormone receptor gene and
RT demonstration of a partial gene deletion in two patients with Laron-
RT type dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8083-8087(1989).
RN [3]
RX DISULFIDE BONDS.
RX MEDLINE=90153957; PubMed=2406245;
RA Fuh G., Mulkerrin M.G., Bass S., McFarland N., Brochier M.,
RA Bourrel J.H., Light D.R., Wells J.A.;
RT "The human growth hormone receptor: Secretion from Escherichia coli
RT and disulfide bonding pattern of the extracellular binding domain.";
RL J. Biol. Chem. 265:3111-3115(1990).
RN [4]
RX VARIANT LARON DWARFISM SER-114.
RX MEDLINE=89384829; PubMed=2779634;
RA Amsellem S., Duquesnoy P., Attree O., Novelli G., Bousnina S.,
RA Postelvinay M.-C., Goossens M.;
RT "Laron dwarfism and mutations of the growth hormone-receptor gene.";
RL New Engl. J. Med. 321:989-995(1989).
RN [5]
RX VARIANTS LARON DWARFISM.
RX MEDLINE=93278381; PubMed=8504296;
RA Amsellem S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
RA Valleix S., Goossens M.;
RT "Spectrum of growth hormone receptor mutations and associated
RT haplotypes in Laron syndrome.";
RL Hum. Mol. Genet. 2:355-359(1993).
RN [6]
RX VARIANT LARON DWARFISM HIS-170.
RX MEDLINE=94185645; PubMed=8137822;
```


GHR_RABIT STANDARD; PRT; 638 AA.

AC PI9341; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE protein).

GN GHR.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RP MEDLINE=88065936; PubMed=2825030;

RX Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Hensel W.J., Barnard R., Waters M.J., Wood W.I.;

RA "Growth hormone receptor and serum binding protein: purification, cloning and expression.";

RT Nature 330:537-543(1987).

RL Nature 330:537-543(1987).

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF015252; AAB67613.1; -.

DR PIR; S08544; B28176.

DR HSP; P10912; I422.

DR InterPro; IPR002996; CR1A.

DR InterPro; IPR003961; FN III.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 18

FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.

FT DOMAIN 19 264 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 265 288 POTENTIAL.

FT DOMAIN 289 638 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 145 252 FIBRONECTIN TYPE-III.

FT DISULFID 56 66 BY SIMILARITY.

FT DISULFID 101 112 BY SIMILARITY.

FT DISULFID 126 140 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 638 AA; 71076 MW; E05CCELD7294624C CRC64;

Query Match 100.0%; Score 65; DB 1; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVFIELDI 12

Db 339 DDSWVFIELDI 350

RESULT 7
GHR_RAT

GHR_RAT STANDARD; PRT; 638 AA.

AC PI6310; 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE protein).

GN GHR.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1] SEQUENCE FROM N.A.

RP MEDLINE=89255563; PubMed=2722883;

RX Mathews L.S., Emberg B., Norstedt G.;

RA "Regulation of rat growth hormone receptor gene expression.";

RL J. Biol. Chem. 264:9905-9910(1989).

RN [2] SEQUENCE FROM N.A.

RP MEDLINE=90006741; PubMed=2792761;

RX Baumbach W.R., Horner D.L., Logan J.S.;

RA "The growth hormone-binding protein in rat serum is an alternatively spliced form of the rat growth hormone receptor.";

RT Genes Dev. 3:1199-1205(1989).

RL Genes Dev. 3:1199-1205(1989).

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; J04811; AAA41219.1; -.

DR PIR; A32985; A33505.

DR HSP; P10912; I422.

DR InterPro; IPR002996; CR1A.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003528; Hemtopoptn_L_F1.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 18

FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.

FT DOMAIN 19 265 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 266 289 POTENTIAL.

FT DOMAIN 290 638 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 145 252 FIBRONECTIN TYPE-III.

FT DISULFID 56 66 BY SIMILARITY.

FT DISULFID 101 112 BY SIMILARITY.

FT DISULFID 126 140 BY SIMILARITY.

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 638 AA; 71236 MW; 0D8E9AF759A21A3B CRC64;

Query Match 100.0%; Score 65; DB 1; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVFIELDI 12

Db 340 DDSWVFIELDI 351


```

RESULT 9
GHR CHICK
ID - GHR CHICK STANDARD; PRT; 608 AA.
AC Q02092;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91243665; PubMed=2036984;
RA Burnside J., Liou S.S., Cogburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens."
RL Endocrinology 128:3183-3192(1991).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Broad specificity.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M74057; AAA48781.1; -.
CC PIR; S32823; S32823.
CC HSSP; P10912; IAXI.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_Fl.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L_Fl; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 608 GROWTH HORMONE RECEPTOR.
FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 261 POTENTIAL.
FT DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 72 83 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 90.8%; Score 59; DB 1; Length 608;
Best Local Similarity 91.7%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDSWVEFIEDI 12
Db 312 DDLWVEFIEDI 323

```

```

RESULT 10
GHR COLLI
ID - GHR COLLI STANDARD; PRT; 611 AA.
AC Q90375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Columba livia (Domestic pigeon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsai K.W.K., Lau K.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U20353; AAA84745.1; -.
CC HSSP; P10912; IAXI.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_Fl.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L_Fl; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.
FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 264 POTENTIAL.
FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 226 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 100 114 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 611 AA; 68851 MW; C48750BF9EB4EBDA CRC64;

Query Match 90.8%; Score 59; DB 1; Length 611;
Best Local Similarity 91.7%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDSWVEFIEDI 12
Db 315 DDLWVEFIEDI 326

```

RESULT 11

RPOC_PSEPU STANDARD; PRT; 1409 AA.

AC P19176;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE DNA-directed RNA polymerase beta' chain (EC 2.7.6) (Transcriptase beta' chain) (RNA polymerase beta' subunit).

DE RPOC.

OS Pseudomonas putida.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=303;

RN [1]

RN SEQUENCE FROM N.A.

RA Danilovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M., Chernov I.P., Azhikina T.L., Monastyrskaya G.S., Sverdlov E.D.;

RT "Nucleotide sequence of the rpoC gene coding for the beta'-subunit of RNA polymerase in Pseudomonas putida.";

RL Dokl. Biochem. 303:241-245(1988).

RN [2]

RN SEQUENCE OF 1-497 FROM N.A.

RX MEDLINE=89117617; PubMed=3219133;

RA Borodin A.M., Danilovich A.V., Chernov I.P., Azhikina T.L., Rostapshov V.M., Monastyrskaya G.S.;

RT "Genes coding for RNA polymerase in bacteria. III. The use of modified Sanger's method for sequencing the C-terminal region of rpoB gene, N-terminal region of rpoC gene and intercistron region of RNA polymerase in Pseudomonas putida.";

RL Bioorg. Khim. 14:1179-1182(1988).

CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + [RNA](N).

CC -1- SUBUNIT: The enzyme consists of the sigma chain and the core enzyme which is composed of 2 alpha chains, 1 beta chain, and 1 beta' chain.

CC -1- SIMILARITY: Belongs to the RNA polymerase beta' chain family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; X16538; CAA34538.1; -

DR EMBL; M38319; AAA25987.1; -

DR PIR; JN0420; JN0420.

DR HSSP; Q9KWU6; 1HQM.

DR InterPro; IPR000722; RNA_pol_A.

DR InterPro; IPR007080; RNA_pol_Rpb1_1.

DR InterPro; IPR007066; RNA_pol_Rpb1_3.

DR InterPro; IPR007083; RNA_pol_Rpb1_4.

DR InterPro; IPR007081; RNA_pol_Rpb1_5.

DR InterPro; IPR006592; RNA_pol_N.

DR Pfam; PF04997; RNA_pol_Rpb1_1; 1.

DR Pfam; PF00623; RNA_pol_Rpb1_2; 1.

DR Pfam; PF04983; RNA_pol_Rpb1_3; 1.

DR Pfam; PF05000; RNA_pol_Rpb1_4; 1.

DR Pfam; PF04998; RNA_pol_Rpb1_5; 1.

DR SMART; SM00663; RPOLA_N; 1.

KW Transference; DNA-directed RNA polymerase; Transcription.

FT CONFLICT 2 2 P -> L (IN REF. 2).

FT CONFLICT 17 17 N -> I (IN REF. 2).

FT CONFLICT 89 89 L -> V (IN REF. 2).

FT CONFLICT 203 203 I -> T (IN REF. 2).

FT CONFLICT 328 328 I -> T (IN REF. 2).

FT CONFLICT 335 335 L -> S (IN REF. 2).

FT CONFLICT 348 348 L -> R (IN REF. 2).

FT CONFLICT 482 482 P -> L (IN REF. 2).

FT CONFLICT 484 484 T -> I (IN REF. 2).

SQ SEQUENCE 1409 AA; 154544 MW; C5662109D3BE3D81 CRC64;

Query Match 73.8%; Score 48; DB 1; Length 1409;

Best Local Similarity 72.7%; Pred. No. 1.8;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDSWVERIELD 11

Db 876 DEQWVEFIEN 886

RESULT 12

SSP2_BOMMO STANDARD; PRT; 704 AA.

AC SP22_BOMMO

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Sex-specific storage-protein 2 precursor.

GN SP2.

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;

OC Bombycidae; Bombyx.

OX NCBI_TaxID=7091;

RN [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=89291839; PubMed=2544581;

RA Fujii T., Sakurai H., Izumi S., Tomino S.;

RT "Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mori.";

RL J. Biol. Chem. 264:11020-11025(1989).

CC -1- FUNCTION: Larval storage protein (LSP) which may serve as a store of amino acids for synthesis of adult proteins.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Fat body.

CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M24370; AAA27848.1; -

DR EMBL; M24371; AAA27848.1; JOINED.

DR PIR; A34287; A34287.

DR HSSP; P04253; 1QXY.

DR InterPro; IPR008922; Di-copper_centre.

DR InterPro; IPR000896; Hemocyanin.

DR InterPro; IPR005203; hemocyanin_C.

DR InterPro; IPR005204; hemocyanin_N.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00372; hemocyanin; 1.

DR Pfam; PF03723; hemocyanin_C; 1.

DR Pfam; PF03722; hemocyanin_N; 1.

DR PRINTS; PR00187; HAEMOCYANIN.

DR PROSITE; PS00209; HEMOCYANIN.

DR PROSITE; PS00210; HEMOCYANIN_1; 1.

DR PROSITE; PS00210; HEMOCYANIN_2; 1.

KW Signal; Storage protein; Glycoprotein.

FT SIGNAL 1 16

FT CHAIN 17 704 SEX-SPECIFIC STORAGE-PROTEIN 2.

FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 704 AA; 83466 MW; 365E7DFE707137EB CRC64;

Query Match 66.2%; Score 43; DB 1; Length 704;

Best Local Similarity 54.5%; Pred. No. 6.6;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELD 11
Db 543 EDNMKPFELD 553

RESULT 13

Y4FP_RHISN STANDARD; PRT; 358 AA.
ID Y4FP_RHISN
AC P55454;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Probable ABC transporter periplasmic binding protein Y4FP precursor.
GN Y4FP.
OS Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.
RT "Molecular basis of symbiosis between Rhizobium and legumes."
RL Nature 387:394-401(1997).
CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM Y4FNOF.
CC -1- SUBCELLULAR LOCATION: Periplasmic (potential).
CC -1- SIMILARITY: SOME, TO S.MARCESCENS IRON(III)-BINDING PERIPLASMIC
CC PROTEIN AND TO H.INFLUENZAE HI0131.
CC -1- CAUTION: It is uncertain whether Met-1 is the initiator.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: AE000073; AAB91672.1; -
DR InterPro; IPR006059; SBP_bac_1.
DR Pfam; PF01547; SBP_bac_1; 1.
KW Hypothetical protein; Transport; Periplasmic; Signal; Plasmid.
FT SIGNAL 1 46 OR 34, OR 40, OR 41 (POTENTIAL).
FT CHAIN 47 358 PROBABLE ABC TRANSPORTER PERIPLASMIC
FT BINDING PROTEIN Y4FP.
SQ SEQUENCE 358 AA; 39015 MW; B485BC3FA3B4D229 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 358;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DDSWVEFIELDI 12
Db 346 DSWLQKIELEI 356

RESULT 14

VGR3_MOUSE STANDARD; PRT; 1363 AA.
ID VGR3_MOUSE
AC P35917;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
DE (VEGFR-3) (tyrosine-protein kinase receptor FLT4).
GN FLT4 OR FLT-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RC MEDLINE=93330572; PubMed=8393164;
RA Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,
RA Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.;
RT "Molecular cloning of murine FLT and FLT4."
RL Oncogene 8:2293-2298(1993).
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
CC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN
CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.
CC CSP-1/PDGF receptor subfamily.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: L07296; AAA40077.1; -
DR PIR; I58375; I58375.
DR HSP; P11362; IFGK.
DR MGD; MGI:95561; Flt4.
DR GO; GO:0005515; F:protein binding; IPI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001824; RecepttyrkinIII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008286; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 5.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00219; TykKc; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
KW Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 1363 VASCULAR ENDOTHELIAL GROWTH FACTOR
FT RECEPTOR 3.
FT DOMAIN 25 775 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 776 797 POTENTIAL.
FT DOMAIN 798 1363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 118 IG-LIKE C2-TYPE 1.
FT DOMAIN 151 213 IG-LIKE C2-TYPE 2.
FT DOMAIN 230 326 IG-LIKE C2-TYPE 3.
FT DOMAIN 331 415 IG-LIKE C2-TYPE 4.
FT DOMAIN 422 552 IG-LIKE C2-TYPE 5.
FT DOMAIN 555 671 IG-LIKE C2-TYPE 6.
FT DOMAIN 678 764 IG-LIKE C2-TYPE 7.
FT DOMAIN 845 1173 PROTEIN KINASE.
FT NP_BIND 851 859 ATP (BY SIMILARITY).
FT BINDING 879 879 ATP (BY SIMILARITY).
FT ACT_SITE 1037 1037 BY SIMILARITY.
FT DISULFID 51 111 POTENTIAL.
FT DISULFID 158 206 POTENTIAL.
FT DISULFID 252 310 POTENTIAL.

```
FT DISULFID 445 534 POTENTIAL.
FT DISULFID 578 653 POTENTIAL.
FT DISULFID 699 751 POTENTIAL.
FT MOD RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1363 AA; 153015 MW; F1BF8A2BDEF99BE9 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 1363;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DSWVEFIE 9
Db 505 DSWTEFVE 512

RESULT 15
SR09_MAIZE
ID -SR09_MAIZE STANDARD; PRT; 103 AA.
AC 004438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal recognition particie 9 kDa protein (SRP9).
GN SRP9.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W64A2;
RA Bui N., Wolff N., Strub K.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Signal-recognition-particle assembly has a crucial role
CC in targeting secretory proteins to the rough endoplasmic reticulum
CC membrane. SRP9 together with SRP14 and the Alu portion of the SRP
CC RNA, constitutes the elongation arrest domain of SRP. The complex
CC of SRP9 and SRP14 is required for SRP RNA binding (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the SRP9 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y10117; CAA71203.1; -.
CC PIR; T03951; T03951.
CC DR HSPP; P49962; 1914.
CC DR InterPro; IPR008832; SRP9.
CC DR InterPro; IPR009018; SRP9/14.
CC DR Pfam; PF05486; SRP9; 1.
CC KW Signal recognition particle; RNA-binding.
SQ SEQUENCE 103 AA; 12077 MW; B6EFA49DA77C13BE CRC64;

Query Match 60.0%; Score 39; DB 1; Length 103;
```

```
Best Local Similarity 54.5%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DSWVEFIELDI 12
Db 5 DSWEEFVERSV 15

Search completed: June 9, 2004, 15:49:05
Job time : 9.75676 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 40.2162 Seconds

(without alignments)
94.147 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:**
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	101	6	Q863n9 arctonx co
2	65	100.0	105	6	Q863q6 lontra cana
3	65	100.0	105	6	Q863p4 eira barbar
4	65	100.0	106	6	Q863q3 lutra lutra
5	65	100.0	106	6	Q863q2 lutra macul
6	65	100.0	107	6	Q863q9 aonyx capen
7	65	100.0	107	6	Q863q8 amblyonx ci
8	65	100.0	107	6	Q863q7 enhydra lut
9	65	100.0	107	6	Q863q5 lontra feli
10	65	100.0	107	6	Q863q4 lontra long
11	65	100.0	107	6	Q863q1 preronura b
12	65	100.0	107	6	Q863q0 mustela erm
13	65	100.0	107	6	Q863p9 mustela fire
14	65	100.0	107	6	Q863p8 mustela vis
15	65	100.0	107	6	Q863p7 martes amer
16	65	100.0	107	6	Q863p6 martes penn

17	65	100.0	107	6	Q863p5 gulo gulo (
18	65	100.0	107	6	Q863p2 ictonyx str
19	65	100.0	107	6	Q863p1 meles meles
20	65	100.0	107	6	Q863p0 taxidea tax
21	65	100.0	107	6	Q863n8 melogale mo
22	65	100.0	107	6	Q863n7 basariscus
23	65	100.0	107	6	Q863n6 procyon lot
24	65	100.0	130	11	Q99MY7 meriones un
25	65	100.0	233	6	Q95MM1 ochotona pr
26	65	100.0	238	11	Q924F8 perognathus
27	65	100.0	293	6	Q8MJM2 elephatulus
28	65	100.0	294	6	Q95ML9 sylvilagus
29	65	100.0	294	6	Q8MJL9 ursus ameri
30	65	100.0	295	6	Q95ML8 tupaia bela
31	65	100.0	295	11	Q80Z48 ctenomys st
32	65	100.0	296	11	Q924F4 hystrix afr
33	65	100.0	296	11	Q924F1 chinchilla
34	65	100.0	296	11	Q924E8 proechimys
35	65	100.0	296	11	Q924E2 thryonomys
36	65	100.0	296	11	Q924E9 dinomys bra
37	65	100.0	296	11	Q924F0 erethizon d
38	65	100.0	296	11	Q80Z55 aconaemys p
39	65	100.0	296	11	Q80Z54 aconaemys s
40	65	100.0	296	11	Q80Z53 octodon bri
41	65	100.0	296	11	Q80Z52 octodontomys
42	65	100.0	296	11	Q80Z51 spalacopus
43	65	100.0	296	11	Q80Z49 tympanoctom
44	65	100.0	296	11	Q80Z47 aconaemys f
45	65	100.0	296	11	Q80Z46 chinchilla

ALIGNMENTS

RESULT 1

ID Q863n9 PRELIMINARY; PRT; 101 AA.
AC Q863n9, 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Arctonx collaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Arctonx.
CX NCBI_TaxID=139309;
RN [1]
RP SEQUENCE FROM N.A.
RA Keepfli K.-P., Wayne R.K.;
RT "Type-1 SIS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498204; AAP19695.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 101 101
SQ SEQUENCE 101 AA; 11428 MW; AD696CB6E0EBD7AC CRC64;

Query Match 100.0%; Score 65; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DDSWVEFIELDI 12

Db 24 DDSWVEFIELDI 35

RESULT 2

OY 1 DDSWVEFIELDI 12
Db 24 DDSWVEFIELDI 35
ID Q863Q6 PRELIMINARY; PRT; 105 AA.

```

AC Q863Q6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra canadensis (River otter) (Lutra canadensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=76717;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498187; AAP19678.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11852 MW; F07A7052451EB8E7 CRC64;

Query Match 100.0%; Score 65; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 28 DDSWVEFIELDI 39

RESULT 3
Q863P4
ID Q863P4 PRELIMINARY; PRT; 105 AA.
AC Q863P4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Eira barbara (Tayra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Eira.
OX NCBI_TaxID=204263;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498199; AAP19690.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11879 MW; F6F6445250DB79BF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 28 DDSWVEFIELDI 39

RESULT 4
Q863Q3
ID Q863Q3 PRELIMINARY; PRT; 106 AA.
AC Q863Q3;

```

```

DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra lutra (European river otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lutra.
OX NCBI_TaxID=9657;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498130; AAP19681.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 12006 MW; EFB0C6D8793AE9FF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 29 DDSWVEFIELDI 40

RESULT 5
Q863Q2
ID Q863Q2 PRELIMINARY; PRT; 106 AA.
AC Q863Q2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra maculicollis (spotted necked otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lutra.
OX NCBI_TaxID=76719;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498191; AAP19682.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 12003 MW; EFB0DDAE24C29FF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 29 DDSWVEFIELDI 40

RESULT 6
Q863Q9
ID Q863Q9 PRELIMINARY; PRT; 107 AA.
AC Q863Q9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)

```

```

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Anonyx capensis (Cape clawless otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Anyx.
OX NCBI_TaxID=76722;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498184; AAPI9675.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12101 MW; 7F3D579D3C26011B CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 7
Q863Q8 ID Q863Q8 PRELIMINARY; PRT; 107 AA.
AC Q863Q8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Amblyonyx cinereus (Asian small-clawed otter) (Anonyx cinereus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Amblyonyx.
OX NCBI_TaxID=55043;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498185; AAPI9676.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 8
Q863Q7 ID Q863Q7 PRELIMINARY; PRT; 107 AA.
AC Q863Q7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

```

```

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Enhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498186; AAPI9677.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12151 MW; 84DD579D3C2EA9FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 9
Q863Q5 ID Q863Q5 PRELIMINARY; PRT; 107 AA.
AC Q863Q5;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra felina (Sea cat) (Lutra felina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=76718;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498188; AAPI9679.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 10
Q863Q4 ID Q863Q4 PRELIMINARY; PRT; 107 AA.
AC Q863Q4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

```

```

DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=71113;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498189; AAP19680.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12166 MW; 9113E146451EA8BB CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 11
Q86301
ID Q863Q1 PRELIMINARY; PRT; 107 AA.
AC Q863Q1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Pteronura brasiliensis (Giant otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Pteronura.
OX NCBI_TaxID=9672;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498192; AAP19683.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12137 MW; 96DBCA309E7789FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 12
Q863Q0
ID Q863Q0 PRELIMINARY; PRT; 107 AA.
AC Q863Q0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

```

```

GN GHR.
OS Mustela erminea (Ermine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=36723;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498193; AAP19684.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 13
Q863P9
ID Q863P9 PRELIMINARY; PRT; 107 AA.
AC Q863P9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Mustela frenata (Long-tailed weasel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=55048;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498194; AAP19685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 14
Q863P8
ID Q863P8 PRELIMINARY; PRT; 107 AA.
AC Q863P8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

```

OS Mustela vison (American mink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Mustela.
 OX NCBI_TaxID=9667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koepfli K.-P., Wayne R.K.;
 RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
 RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
 RL Syst. Biol. 0:0-0(2003).
 DR EMBL; AF498195; AAP19686.1; -.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 12149 MW; 96CCE146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
 |||||
 Db 30 DDSWVEFIELDI 41

RESULT 15
 Q863P7
 ID Q863P7 PRELIMINARY; PRT; 107 AA.
 AC Q863P7;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Growth hormone receptor (Fragment).
 GN GHR.
 OS Martes americana (American marten).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
 OC Martes.
 OX NCBI_TaxID=9660;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Koepfli K.-P., Wayne R.K.;
 RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
 RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
 RL Syst. Biol. 0:0-0(2003).
 DR EMBL; AF498196; AAP19687.1; -.
 KW Receptor.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 12172 MW; 96DBD14658B649FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
 |||||
 Db 30 DDSWVEFIELDI 41

Search completed: June 9, 2004, 15:51:22
 Job time : 40.2162 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 50 Seconds
(without alignments)
56.510 Million cell updates/sec

Title: US-09-660-302D-3
Perfect score: 55
Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1596107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1596107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	55	100.0	12	2 AAY32789	Aay32789 Growth ho
2	55	100.0	130	2 AAY32792	Aay32792 Growth ho
3	55	100.0	637	1 AAP92108	Aap92108 Human gro
4	55	100.0	638	1 AAP81326	Aap81326 Human gro
5	55	100.0	638	1 AAP81327	Aap81327 Rabbit gr
6	55	100.0	638	1 AAP92107	Aap92107 Rabbit gr
7	55	100.0	638	2 AAW33394	Aaw33394 Human gro
8	55	100.0	638	2 AAW33395	Aaw33395 Rabbit gr
9	55	100.0	638	7 ADD45061	Add45061 Rat Prote
10	55	100.0	638	7 ADD45067	Add45067 Human pro
11	55	100.0	638	7 ADD45063	Add45063 Human pro
12	55	100.0	638	7 ADD45065	Add45065 Rat Prote
13	55	100.0	648	4 ABB11437	Abb11437 Human gro
14	51	92.7	638	2 AAR06473	Aar06473 Serum som
15	49	89.1	12	2 AAY32793	Aay32793 Growth ho
16	49	89.1	12	2 AAY32794	Aay32794 Chicken g
17	49	89.1	608	2 AAR25246	Aar25246 Chicken G
18	43	78.2	705	5 ABB77350	Abb77350 Plodia in
19	42	76.4	1399	6 ABU41685	Abu41685 Protein e
20	42	76.4	1409	6 ABU39890	Abu39890 Protein e
21	40	72.7	1363	4 AAB37607	Aab37607 Human pro
22	40	72.7	1363	6 ABU04285	Abu04285 Human exp
23	39	70.9	14	6 ADA09064	Ada09064 Lanthanid
24	39	70.9	163	2 AAW20448	Aaw20448 H. pylori
25	39	70.9	255	3 AAB53166	Aab53166 Macaca mu

ALIGNMENTS

RESULT 1

AAY32789

ID AAY32789 standard; peptide; 12 AA.

XX AC AAY32789;

XX DT 09-NOV-1999 (first entry)

XX DE Growth hormone receptor polypeptide for inhibition of receptor cleavage.

XX KW Growth hormone receptor; signal transduction; proteolytic cleavage;

XX KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;

XX KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS.

XX OS Mammalia.

XX PN EP943624-AL.

XX PD 22-SEP-1999.

XX PF 12-MAR-1998; 98EP-00200799.

XX PR 12-MAR-1998; 98EP-00200799.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX DR WPI; 1999-510566/43.

XX PT Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

XX PS Claim 11; Page 27; 36pp; English.

XX CC This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, of which this sequence is an example, is located at or around a ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

CC stress and during neuromuscular disease

XX Sequence 12 AA;

Query Match 100.0%; Score 55; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
|||||
Db 2 DSWVEFIELD 11

RESULT 2

ID AAY32792 standard; peptide; 130 AA.

AC AAY32792;

XX 09-NOV-1999 (first entry)

XX Growth hormone receptor polypeptide.

XX Signal transduction; proteolytic cleavage; growth hormone receptor;
KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;
KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
KW growth hormone deficiency.

XX Mammalia.

XX EP943624-A1.

XX 22-SEP-1999.

XX 12-MAR-1998; 98EP-00200799.

XX 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

XX Controlling the availability and/or signal transduction capability of a
PT cell surface receptor, useful for treating growth hormone deficiencies.

XX Disclosure; Page 5; 36pp; English.

XX This sequence is a growth hormone receptor polypeptide. Polypeptides for
CC the upregulation of the growth hormone receptor are derived from this
CC sequence e.g. AAY32793. Variants (AAY32794-Y32823) of the derived
CC sequence are examples of polypeptide sequences found at or near the
CC ubiquitin/proteosome binding site located on the intracellular part of a
CC cell surface receptor. These sequences are used in a method for
CC controlling the availability and signal transduction capability of a cell
CC surface receptor by administering an inhibitor that is capable of
CC inhibiting proteolytic cleavage of the receptor. Inhibition of this
CC proteolytic cleavage results in the receptors being present on the
CC surface for longer and therefore signalling for longer to the interior of
CC the cell. This increases the sensitivity of cells to any hormones which
CC might be present. The inhibitor is either derived from, competes with or
CC binds to a polypeptide sequence of which sequences AAY32794-Y32823 are
CC examples. The inhibitor may be used to treat muscle wasting, associated
CC with disorders such as renal tubular defects, uraemia, diabetes,
CC Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and
CC during neuromuscular disease

XX Sequence 130 AA;

Query Match 100.0%; Score 55; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

Db 53 DSWVEFIELD 62
|||||

RESULT 3

AAP92108
ID AAP92108 standard; protein; 637 AA.

XX AAP92108;

XX 14-FEB-1990 (first entry)

XX Human growth hormone receptor.

XX Growth hormone receptor.

XX Homo sapiens.

XX US4857637-A.

XX 15-AUG-1989.

XX 12-JUN-1987; 87US-00061942.

XX 22-MAY-1985; 85US-00737302.

XX 07-MAY-1986; 86US-00861236.

XX (GETH) GENENTECH INC.

XX Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;

XX WPI; 1989-300419/41.

XX N-PSDB; AAN91325.

XX Modulating growth hormone receptor activity - by immunising animal
PT against growth hormone receptor extracellular domain deriv. to raise
PT antiserum.

XX Disclosure; Fig 2a-c; 18pp; English.

XX An animal can be immunised against its growth hormone receptor by
CC vaccinating against a growth hormone receptor extracellular domain deriv.
CC predetermined to raise polyclonal antisera which affect the receptor as a
CC growth hormone agonist. This method enables continuous growth of target
CC tissues without frequent hormone admin

XX Sequence 637 AA;

Query Match 100.0%; Score 55; DB 1; Length 637;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

Db 340 DSWVEFIELD 349

RESULT 4

AAP81326
ID AAP81326 standard; protein; 638 AA.

XX AAP81326;

XX 23-OCT-1990 (first entry)

XX Human growth hormone receptor.

XX Growth hormone receptor; gigantism; acromegaly.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1. .18

```

FT XX /label= signal_sequence
PN XX
XX WO809818-A.
XX
XX 15-DEC-1988.
XX
XX 10-JUN-1988; 88WO-US002008.
XX
XX 12-JUN-1987; 87US-00062542.
XX
XX (GETH ) GENENTECH INC.
XX
XX Hammonds RG, Leungh D, Wood WI;
XX
XX WPI; 1988-368632/51.
XX
XX N-PSDB; AAN81716.
XX
XX New pure growth hormone receptor and binding protein - for treating
PT growth hormone abnormalities, and new encoding DNA sequences.
XX
XX Disclosure; Page ?; lpp; English.
XX
XX The sequence was deduced from a clone isolated from an adult liver cDNA
CC lambda gt10 library. The DNA can be inserted into an expression vector
CC for prodn. of the recombinant GHR which is used to treat GH-related
CC disorders such as gigantism and acromegaly. A hydropathy plot revealed an
CC extracellular GH binding domain, a transmembrane domain, and an
CC intracellular signalling domain. Eight potential N-linked glycosylation
CC sites are predicted. See also AAP81327 and AAN81718-9
XX
XX Sequence 638 AA;
SQ
Query Match 100.0%; Score 55; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 340 DSWVEFIELD 349
|||||
RESULT 5
AAP81327
ID AAP81327 standard; protein; 638 AA.
XX
XX AAP81327;
AC
XX
XX 13-FEB-1990 (first entry)
DT
XX
XX Rabbit growth hormone receptor.
DE
XX
XX Growth hormone receptor; rabbit.
KW
XX
XX Oryctolagus cuniculus.
OS
XX
XX US4857637-A.
PN
XX
XX 15-AUG-1989.
PD
XX
XX 12-JUN-1987; 87US-00061942.
PF
XX
XX 22-MAY-1985; 85US-00737302.
PR
XX
XX 07-MAY-1986; 86US-00861236.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX
XX Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;
PI
XX
XX WPI; 1989-300419/41.
XX
XX N-PSDB; AAN91323.
DR
XX
XX Modulating growth hormone receptor activity - by immunising animal
PT against growth hormone receptor extracellular domain deriv. to raise
FT antiser.
XX
XX Disclosure; Fig 1a-c; 18pp; English.
PS
XX
XX An animal can be immunised against its growth hormone receptor by
CC vaccinating against a growth hormone receptor extracellular domain deriv.
CC predetermined to raise polyclonal antisera which affect the receptor as a
CC growth hormone agonist. This method enables continuous growth of target
CC tissues without frequent hormone admin
XX
XX Sequence 638 AA;
SQ
Query Match 100.0%; Score 55; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 340 DSWVEFIELD 349
|||||
RESULT 5
AAP81327
ID AAP81327 standard; protein; 638 AA.
XX
XX AAP81327;
AC
XX
XX 23-OCT-1990 (first entry)
DT
XX
XX Rabbit growth hormone receptor.
DE
XX
XX Growth hormone receptor; rabbit; gigantism; acromegaly.
KW
XX
XX Oryctolagus cuniculus.
OS
XX
XX Key Location/Qualifiers
FH 1. 18
FT Peptide /label= signal_sequence
XX
XX WO809818-A.
PN
XX
XX 15-DEC-1988.
PD
XX
XX 10-JUN-1988; 88WO-US002008.
PF
XX
XX 12-JUN-1987; 87US-00062542.
PR
XX
XX (GETH ) GENENTECH INC.
XX
XX Hammonds RG, Leungh D, Wood WI;
XX
XX WPI; 1988-368632/51.
XX
XX N-PSDB; AAN81717.
XX

```

Qy 1 DSWVEFIELD 10
 |||||
 Db 340 DSWVEFIELD 349

RESULT 7
 AAW33394
 ID AAW33394 standard; protein; 638 AA.

XX AC AAW33394;
 XX 25-MAR-2003 (revised)
 DT 11-MAY-1998 (first entry)
 XX Human growth hormone receptor.

XX Growth hormone receptor; growth hormone binding protein; somatotropin;
 KW human; gigantism; acromegaly; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Sig_peptide
 FT Domain 247..269
 FT /note= "transmembrane domain"
 FT Misc-difference 375
 FT /note= "translated codon is Ser in clone ghr.210 and
 FT ghr.110, Ile in ghr.501"

XX US5688763-A.

XX 18-NOV-1997.

XX 25-MAY-1994; 94US-00248832.

XX 12-JUN-1987; 87US-00062542.

XX 28-JUN-1991; 91US-00723358.

XX 08-JAN-1993; 93US-00002489.

XX (LEUN/) LEUNG D W.

XX (HAMM/) HAMMONDS R G.

XX (WOOD/) WOOD W I.

XX (COLO/) COLOSI P C.

XX (SPEN/) SPENCER S A.

XX Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;

XX WPI; 1998-008010/01.

XX N-PSDB; AAT94063.

XX Human and rabbit growth hormone receptor protein - useful to treat
 PT disorders associated with overexpression, e.g. gigantism and acromegaly.

XX Claim 2; Fig 8a; 60pp; English.

XX This protein sequence comprises human growth hormone receptor. The amino
 CC acid sequence was deduced from cDNA clones (see AAT94063) obtained from a
 CC human liver cDNA library, and shows 84% identity to the rabbit growth
 CC hormone receptor (see AAW33394). Human growth hormone receptor, its
 CC derivatives in which the cytoplasmic or transmembrane domains are
 CC deleted, and growth hormone binding proteins comprising amino acids 190-
 CC 246 or 1-324 of the mature protein, can be used to treat disorders
 CC associated with growth hormone over-expression, e.g. gigantism and
 CC acromegaly. The binding protein may also be used to increase the
 CC stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
 CC to correct PF field.)

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.71;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
 |||||
 Db 340 DSWVEFIELD 349

RESULT 8
 AAW33395
 ID AAW33395 standard; protein; 638 AA.

XX AC AAW33395;

XX 25-MAR-2003 (revised)

DT 11-MAY-1998 (first entry)

XX Rabbit growth hormone receptor.

XX Growth hormone receptor; growth hormone binding protein; somatotropin;
 KW rabbit; gigantism; acromegaly; therapy.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers
 FT Peptide 1..18
 FT /label= Sig_peptide
 FT Misc-difference 49

FT /note= "translated codon is Ala in clone ghr.435, Thr in
 FT ghr.440"

FT Domain 247..269

FT /note= "transmembrane domain"

XX US5688763-A.

XX 18-NOV-1997.

XX 25-MAY-1994; 94US-00248832.

XX 12-JUN-1987; 87US-00062542.

XX 28-JUN-1991; 91US-00723358.

XX 08-JAN-1993; 93US-00002489.

XX (LEUN/) LEUNG D W.

XX (HAMM/) HAMMONDS R G.

XX (WOOD/) WOOD W I.

XX (COLO/) COLOSI P C.

XX (SPEN/) SPENCER S A.

XX Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;

XX WPI; 1998-008010/01.

XX N-PSDB; AAT94064.

XX Human and rabbit growth hormone receptor protein - useful to treat
 PT disorders associated with overexpression, e.g. gigantism and acromegaly.

XX Claim 2; Fig 8b; 60pp; English.

XX This protein sequence comprises rabbit growth hormone receptor. The amino
 CC acid sequence was deduced from cDNA clones (see AAT94064) obtained from a
 CC rabbit liver cDNA library, and shows 84% identity to the human growth
 CC hormone receptor (see AAW33394). Rabbit and human growth hormone
 CC receptors, their derivatives in which the cytoplasmic or transmembrane
 CC domains are deleted, and growth hormone binding proteins comprising amino
 CC acids 190-246 or 1-324 of the mature proteins, can be used to treat
 CC disorders associated with growth hormone over-expression, e.g. gigantism
 CC and acromegaly. The binding protein may also be used to increase the
 CC stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
 CC to correct PF field.)

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.71;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10
Best Local Similarity 100.0%; Score 55; DB 7; Length 638;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 340 DSWVERFIELD 349

RESULT 9
ADD45061
ID ADD45061 standard; protein; 638 AA.
XX AC ADD45061;
XX 29-JAN-2004 (first entry)
XX DE Rat Protein P16310, SEQ ID NO 10493.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (PARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI: 2003-268312/26.
XX GENBANK; P16310.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10
Db 341 DSWVERFIELD 350

RESULT 10
ADD45067
ID ADD45067 standard; protein; 638 AA.
XX AC ADD45067;
XX 29-JAN-2004 (first entry)

XX DE Human Protein P10912, SEQ ID NO 10499.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (PARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI: 2003-268312/26.
XX GENBANK; P10912.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;
 Best Local Similarity 100.0%; Pred. No. 0.71; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 DSWVEFIELD 10
 |||||
 Db 340 DSWVEFIELD 349

RESULT 11
 ADD45063
 ID ADD45063 standard; protein; 638 AA.

XX AC ADD45063;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P10912, SEQ ID NO 10495.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P10912.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;
 Best Local Similarity 100.0%; Pred. No. 0.71;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
 |||||
 Db 340 DSWVEFIELD 349

RESULT 12

ADD45065

ID ADD45065 standard; protein; 638 AA.

XX AC ADD45065;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P16310, SEQ ID NO 10497.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P16310.

XX PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more of the

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 341 DSWVEFIELD 350
|||||

RESULT 13

AB11437
ID ABB11437 standard; peptide; 648 AA.
XX
AC ABB11437;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human growth hormone receptor homologue, SEQ ID NO:1807.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytotatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WC200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR N-PSDB; ABA08681.
XX
XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 20; Page 189-190; 1963pp; English.
XX

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activity; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention

XX Sequence 648 AA;

Query Match 100.0%; Score 55; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 350 DSWVEFIELD 359
|||||

RESULT 14

AAR06473
ID AAR06473 standard; protein; 638 AA.
XX
AC AAR06473;
XX
DT 27-AUG-2003 (revised)
DT 04-JAN-1991 (first entry)
XX
XX Serum somatotropin receptor protein from clone pRAT7-12.
XX
XX Somatotropin receptor; SR; somatotropin binding protein; SBP; pRAT7-12;
KW pRAT1-6.
XX
XX Rattus rattus.
OS
XX
XX Key Location/Qualifiers
FT Peptide 1..17 /label= signal_sequence
FT Region 262..638 /label= divergence
FT /note= "non-homology region with SBP/pRAT1-6"
FT Domain 264..289 /label= transmembrane_domain
FT

```

XX EP383205-A.
XX
XX 22-AUG-1990.
XX
XX 09-FEB-1990; 90EP-00102552.
XX
XX 17-FEB-1989; 89US-00310725.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Logan JS, Baumbach WR;
XX WPI; 1990-255493/34.
XX
XX N-PSDB; AAQ05691.
XX
XX Somatotropin binding protein and gene - used to regulate and/or modify
XX activity of somatotropin in humans and animals.
XX
XX Disclosure; Fig 6; 43pp; English.
XX
XX Homology comparison between this putative rat somatotropin receptor and
XX the published sequence indicates 70% identity. See also AAQ05689-91,
XX AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 638 AA;
SQ
Query Match 92.7%; Score 51; DB 2; Length 638;
Best Local Similarity 90.0%; Pred. No. 3.3;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 341 ESWVEFIELD 350

RESULT 15
AAAY32793
ID AAAY32793 standard; peptide; 12 AA.
XX
XX AC AAAY32793;
XX
XX 09-NOV-1999 (first entry)
XX
XX Growth hormone receptor derived polypeptide.
XX
XX Signal transduction; proteolytic cleavage; growth hormone receptor;
XX proteosome binding site; muscle wasting; renal tubular defect; uraemia;
XX diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
XX growth hormone deficiency.
XX
XX Mammalia.
XX
XX EP943624-A1.
XX
XX 22-SEP-1999.
XX
XX 12-MAR-1998; 98EP-00200799.
XX
XX 12-MAR-1998; 98EP-00200799.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
XX
XX WPI; 1999-510568/43.
XX
XX Controlling the availability and/or signal transduction capability of a
XX cell surface receptor, useful for treating growth hormone deficiencies.
XX
XX Disclosure; Page 5; 36pp; English.
XX
XX This sequence is derived from the growth hormone receptor polypeptide
XX AAAY32792. This sequence and variants (AAAY32794-Y32823) of it are examples
XX of polypeptide sequences found at or near the ubiquitin/proteosome

```

```

CC binding site located on the intracellular part of a cell surface
CC receptor. These sequences are used in a method for controlling the
CC availability and signal transduction capability of a cell surface
CC receptor by administering an inhibitor that is capable of inhibiting
CC proteolytic cleavage of the receptor, inhibition of this proteolytic
CC cleavage results in the receptors being present on the surface for longer
CC and therefore signalling for longer to the interior of the cell. This
CC increases the sensitivity of cells to any hormones which might be
CC present. The inhibitor is either derived from, competes with or binds to
CC a polypeptide sequence of which sequences AAAY32794-Y32823 are examples.
CC The inhibitor may be used to treat muscle wasting, associated with
CC disorders such as renal tubular defects, uraemia, diabetes, Cushing's
CC syndrome, cachexias, eating disorders, AIDS, after stress and during
CC neuromuscular disease
XX
XX Sequence 12 AA;
SQ
Query Match 89.1%; Score 49; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 SWVEFIELD 10
Db 1 SWVEFIELD 9

```

Search completed: June 9, 2004, 15:48:27
Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 11.0811 Seconds
(without alignments)
86.807 Million cell updates/sec

Title: US-09-660-302D-3

Perfect score: 55

Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	634	2 S33339	somatotropin recep
2	55	100.0	638	2 A33505	somatotropin recep
3	55	100.0	638	2 A33991	somatotropin recep
4	55	100.0	638	2 B28176	somatotropin recep
5	55	100.0	638	2 S12136	somatotropin recep
6	55	100.0	677	2 S33608	somatotropin-bind
7	49	89.1	608	2 S32823	somatotropin recep
8	46	83.6	702	2 A61619	arylphorin precurs
9	41	74.5	704	2 A34287	storage protein 2
10	41	74.5	1379	2 JC4954	vascular endotheli
11	40	72.7	1363	2 I58375	protein-tyrosine k
12	39	70.9	217	2 AG2426	hypothetical prote
13	39	70.9	321	2 H71924	hypothetical prote
14	39	70.9	321	2 B64589	hypothetical prote
15	39	70.9	411	2 B66916	hypothetical prote
16	38	69.1	103	2 T03951	signal recognition
17	37	67.3	363	2 S75238	hypothetical prote
18	37	67.3	840	2 T36175	probable large ATP
19	37	67.3	1298	2 A48939	protein-tyrosine k
20	36	65.5	208	2 B87468	conserved hypothet
21	36	65.5	243	2 B69951	hypothetical prote
22	36	65.5	268	2 T50354	S-amino-6-(5-phosp
23	36	65.5	316	2 C88448	protein C45G9.5 [i
24	36	65.5	399	2 A97993	nikkomycin biosynt
25	36	65.5	694	2 S67256	probable membrane
26	36	65.5	718	2 T05850	homeobox protein A
27	35	63.6	155	2 S70046	hypothetical prote
28	35	63.6	210	2 S74784	hypothetical prote
29	35	63.6	259	2 A59095	hypothetical prote

30	35	63.6	297	2 G84731	hypothetical prote
31	35	63.6	387	2 T29966	hypothetical prote
32	35	63.6	456	2 T48291	hypothetical prote
33	35	63.6	525	2 S35614	site-specific DNA-
34	35	63.6	537	2 T21823	hypothetical prote
35	35	63.6	544	2 F82557	hypothetical prote
36	35	63.6	555	2 T00778	probable tRNA aden
37	35	63.6	572	2 D95174	phosphoglucosidase
38	35	63.6	572	2 F98040	phosphomannomutase
39	35	63.6	599	2 T45742	crooked neck-like
40	35	63.6	621	2 A57591	ID-associated prot
41	35	63.6	721	2 C84732	probable homeodoma
42	35	63.6	749	2 G86186	hypothetical prote
43	35	63.6	800	2 S13032	3',5'-cyclic-GMP p
44	35	63.6	853	2 A36617	3',5'-cyclic-GMP p
45	35	63.6	854	2 A42828	3',5'-cyclic-GMP p

ALIGNMENTS

RESULT 1

S33339

somatotropin receptor - sheep

N;Alternate names: growth hormone receptor

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 02-Aug-2002

C;Accession: S33339

R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.

Mol. Cell. Endocrinol. 73, 135-145, 1990

A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expr

A;Reference number: S33339; MUID:91099608; PMID:1980117

A;Accession: S33339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-634 <ADA>

A;Cross-references: EMBL:M82912; NID:g165889; PIDN:AAA73171.1; PID:g165889

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

Query Match 100.0%; Score 55; DB 2; Length 634;

Best Local Similarity 100.0%; Pred. NO. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

Db 336 DSWVEFIELD 345

RESULT 2

A33505

somatotropin receptor precursor - rat

N;Alternate names: growth hormone receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 02-Aug-2002

C;Accession: A32985; A33505

R;Baumbach, W.R.; Horner, D.L.; Logan, J.S.

Genes Dev. 3, 1199-1205, 1989

A;Title: The growth hormone-binding protein in rat serum is an alternatively spliced fo

A;Reference number: A32985; MUID:90006741; PMID:2792761

A;Accession: A32985

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <BAU>

A;Cross-references: GB:X16726

R;Mathews, L.S.; Enberg, B.; Norstedt, G.

J. Biol. Chem. 264, 9905-9910, 1989

A;Title: Regulation of rat growth hormone receptor gene expression.

A;Reference number: A33505; MUID:89255563; PMID:2722883

A;Accession: A33505

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <MAT>

A;Cross-references: GB:J04811; NID:g204308; PIDN:AAA41219.1; PID:g204309

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein

Query Match 100.0%; Score 55; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
|||||

Db 341 DSWVEFIELD 350

RESULT 3

A33991
N;Alternate names: somatotropin precursor - human
N;Contains: somatotropin-binding protein, serum
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 02-Aug-2002
C;Accession: A33991; S04530
R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R
Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989
A;Title: Characterization of the human growth hormone receptor gene and demonstration of
A;Reference number: A33991; MUID:90046742; PMID:2813379
A;Accession: A33991
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-638 <GOD>
A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;
Nature 330, 537-543, 1987
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex
A;Reference number: S04530; MUID:88065896; PMID:2825030
A;Accession: S04530
A;Molecule type: mRNA
A;Residues: 1-543; 'I', 545-638 <LEU>
A;Cross-references: EMBL:X06562; NID:G31737; PIDN:CAA29808.1; PID:G31738
C;Genetics:
A;Gene: GDB:GHR
A;Cross-references: GDB:119984; OMIM:600946
A;Map position: 5p13-5p12
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: liver; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-638/Product: somatotropin receptor #status predicted <MAT>
F;265-288/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 55; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
|||||

Db 340 DSWVEFIELD 349

RESULT 4

B28176
somatotropin receptor precursor, hepatic - rabbit
N;Alternate names: growth hormone receptor
N;Contains: somatotropin-binding protein, serum
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Feb-1990 #sequence_revision 10-Mar-1994 #text_change 02-Aug-2002
C;Accession: S08544; B28176; A28176
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;
Nature 330, 537-543, 1987
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex
A;Reference number: S04530; MUID:88065896; PMID:2825030
A;Accession: S08544
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-638 <LEU>
A;Cross-references: GB:AF015252; NID:G2342651; PIDN:AAB67613.1; PID:G2342652

A;Note: part of this sequence, including the amino end of the mature protein, was confi
R;Spencer, S.A.; Hammonds, R.G.; Henzel, W.J.; Rodriguez, H.; Waters, M.J.; Wood, W.I.
J. Biol. Chem. 263, 7862-7867, 1988
A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification,
A;Reference number: A92721; MUID:88227992; PMID:3372509
A;Accession: B28176
A;Molecule type: protein
A;Residues: 19-34; 'SPG', 81-88; 'X', 99; 'XX', 102-105; 'X', 107-110; 'XX', 113-114; 'X', 141; 'X',
-574; 'X', 576-577; 579-595 <SPE>
A;Note: sequence is derived from intact receptor
A;Accession: A28176
A;Molecule type: protein
A;Residues: 'XXX', 22-45; 'X', 47-55 <SP2>
A;Note: sequence is derived from a soluble form of the receptor isolated from serum
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: glycoprotein; liver; transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-638/Product: somatotropin receptor #status experimental <MAT>
F;265-288/Domain: transmembrane #status predicted <TMM>
F;46,200/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 55; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
|||||

Db 340 DSWVEFIELD 349

RESULT 5

S12136
somatotropin receptor precursor - pig
N;Alternate names: growth hormone receptor
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S12136
R;Cioffi, J.A.; Wang, X.; Kopchick, J.J.
Nucleic Acids Res. 18, 6451, 1990
A;Title: Porcine growth hormone receptor cDNA sequence.
A;Reference number: S12136; MUID:91057155; PMID:2243805
A;Accession: S12136
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-638 <C10>
A;Cross-references: EMBL:X54429; NID:G2037; PIDN:CAA38301.1; PID:G2038
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology
C;Keywords: transmembrane protein

Query Match 100.0%; Score 55; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
|||||

Db 340 DSWVEFIELD 349

RESULT 6

S33608
somatotropin-binding protein, high molecular weight, precursor - mouse
N;Alternate names: growth hormone-binding protein, high molecular weight
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Aug-2002
C;Accession: S33608; S33607
R;Smith, W.C.; Kuniyoshi, J.; Talamantes, F.
Mol. Endocrinol. 3, 984-990, 1989
A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular
A;Reference number: S33607; MUID:89295449; PMID:2739661
A;Accession: S33608
A;Molecule type: mRNA
A;Residues: 1-677 <SM1>
A;Cross-references: EMBL:M33324; NID:G193508; PIDN:AAA37690.1; PID:G309253

A;Experimental source: liver

A;Accession: S33607

A;Molecule type: mRNA

A;Residues: 1-324 <SM2>

A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; receptor; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-677/Product: somatotropin-binding protein, high molecular weight #status predicted

F;274-297/Domain: transmembrane #status predicted <TM>

F;40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 55; DB 2; Length 677;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

Db 376 DSWVEFIELD 385

RESULT 7

S32823

somatotropin receptor precursor, major splice form - chicken

N;Alternate names: growth hormone receptor

N;Contains: somatotropin receptor, short form

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 02-Aug-2002

C;Accession: S32823; A49812

R;Burnside, J.; Liou, S.S.; Cogburn, L.A.

Endocrinology 128, 3183-3192, 1991

A;Title: Molecular cloning of the chicken growth hormone receptor complementary deoxyrib

A;Reference number: S32823; MUID:91243665; PMID:2036984

A;Accession: S32823

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-608 <BUR>

A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811

R;Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.

Mol. Endocrinol. 7, 1391-1398, 1993

A;Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf c

A;Reference number: A49812; MUID:94158898; PMID:8114754

A;Accession: A49812

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <HUA>

A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138

A;Experimental source: liver, normal chicken

A;Note: this truncated form is a minor splice form in normal chickens and the major form

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane protei

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-109/Product: somatotropin receptor, short form #status predicted <SHO>

Query Match 89.1%; Score 49; DB 2; Length 608;

Best Local Similarity 90.0%; Pred. No. 0.58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

Db 313 DLWVEFIELD 322

RESULT 8

A61619

arylphorin precursor - greater wax moth

N;Alternate names: phenylalanine-rich protein Lhp76

C;Species: Galleria mellonella (greater wax moth)

C;Date: 21-Jul-1995 #sequence_revision 11-Aug-1995 #text_change 24-Sep-1999

C;Accession: A61619

R;Mummel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.

Insect Biochem. Mol. Biol. 22, 333-342, 1992

A;Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellone

A;Reference number: A61619

A;Accession: A61619

A;Molecule type: DNA

A;Residues: 1-702 <MEM>

A;Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078

A;Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dup

C;Genetics:

A;Introns: 30/1; 74/3; 352/3; 410/2

A;Note: single copy gene

C;Superfamily: arylphorin

C;Keywords: glycoprotein; hemolymph; storage protein

F;1-16/Domain: signal sequence #status predicted <SIG>

F;211,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.6%; Score 46; DB 2; Length 702;

Best Local Similarity 70.0%; Pred. No. 2.3;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

Db 547 DWINFIELD 556

RESULT 9

A34287

storage protein 2 - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 04-Sep-1998

C;Accession: A34287

R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.

J. Biol. Chem. 264, 11020-11025, 1989

A;Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mo

A;Reference number: A34287; MUID:89291839; PMID:2544581

A;Accession: A34287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-704 <FUJ>

C;Superfamily: arylphorin

Query Match 74.5%; Score 41; DB 2; Length 704;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

Db 544 DNMKFFELD 553

RESULT 10

JC4954

vascular endothelial growth factor receptor 2 precursor - Japanese quail

N;Alternate names: Quail endothelial kinase 2; Quek 2

C;Species: Coturnix coturnix japonica (Japanese quail)

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 24-Sep-1999

C;Accession: JC4954

R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.

Gene 174, 3-8, 1996

A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor

A;Reference number: JC4953; MUID:97017121; PMID:8863722

A;Accession: JC4954

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1379 <EIC>

A;Cross-references: EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707416

C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;789-810/Domain: transmembrane #status predicted <TM>

F;856-1188/Domain: protein kinase homology <KIN>

F;864-872/Region: protein kinase ATP-binding motif

Query Match 74.5%; Score 41; DB 2; Length 1379;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIE 8
 |||||
 Db 519 DTWVEFVE 526

RESULT 11

I58375
 C:Species: Mus musculus (house mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 04-Feb-2000
 C:Accession: I58375; B42010
 R:Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J.
 Oncogene 8, 2293-2298, 1993
 A:Title: Molecular cloning of murine FLT and FLT4.
 A:Reference number: I58375; MUID:93330572; PMID:8393164
 A:Accession: I58375
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1363 <RES>
 A:Cross-references: GB:I07296; NID:G293780; PIDN:AAA40077.1; PID:G293781
 R:Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.
 Genomics 13, 475-478, 1992
 A:Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.
 A:Reference number: A42010; MUID:92307693; PMID:11319394
 A:Accession: B42010
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: DNA
 A:Residues: 1033-1072 <GAL>
 C:Genetics:
 A:Gene: FLT4
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
 F:843-1176/Domain: protein kinase homology <KIN>
 F:851-859/Region: protein kinase ATP-binding motif

Query Match 72.7%; Score 40; DB 2; Length 1363;
 Best Local Similarity 75.0%; Pred. No. 57;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSWVEFIE 8
 |||||
 Db 505 DSWTEFVE 512

RESULT 12

AG2426
 C:Species: Nostoc sp. PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AG2426
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-217 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA876666.1; PID:gl7134105; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all4967

Query Match 70.9%; Score 39; DB 2; Length 217;
 Best Local Similarity 87.5%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WVEFIELD 10
 |||||
 Db 182 WVEFIELD 189

RESULT 13

H71924
 C:Species: Helicobacter pylori (strain J99)
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000
 C:Accession: H71924
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
 ; Ives, C.; Gibson, R.; Merberg, D.; Millis, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: H71924
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-321 <ARN>
 A:Cross-references: GB:AE001483; GB:AE001439; NID:94155034; PIDN:AAD06079.1; PID:941550
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp0501
 C:Superfamily: Helicobacter pylori hypothetical protein jhp0501

Query Match 70.9%; Score 39; DB 2; Length 321;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
 |||||
 Db 240 DIWVEVIDLD 249

RESULT 14

B64589
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000
 C:Accession: B64589
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: B64589
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-321 <TOM>
 A:Cross-references: GB:AE000569; GB:AE000511; NID:92313663; PIDN:AAD07620.1; PID:923136
 C:Superfamily: Helicobacter pylori hypothetical protein jhp0501

Query Match 70.9%; Score 39; DB 2; Length 321;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
 |||||
 Db 240 DIWVEVIDLD 249

RESULT 15

S66916
 C:Species: Saccharomyces cerevisiae
 A:Alternate names: N; yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
 C:Accession: S66916
 R:Landt, O.; Hiesel, R.; Unseld, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66907
 A;Accession: S66916
 A;Molecule type: DNA
 A;Residues: 1-411 <LAN>
 A;Cross-references: EMBL:Z74949; NID:gl420165; PID:e251966; PID:gl420167; GSPDB:GN000015;
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: MIPS:YOR042w
 A;Cross-references: SGD:S0005568
 A;Map position: 15R

Query Match 70.9%; Score 39; DB 2; Length 411;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
 ||| :|||
 Db 224 DSWQFVEKD 233

Search completed: June 9, 2004, 15:52:17
 Job time : 12.0811 secs

This Page Blank (uspto)

Result No.	Score	Query		DB	ID	Description
		Match	%			
1	55	100.0	634	1	GHR_BOVIN	P79108 bos taurus
2	55	100.0	634	1	GHR_SHEEP	Q28575 ovis aries
3	55	100.0	638	1	GHR_HUMAN	P10912 homo sapien
4	55	100.0	638	1	GHR_MACMU	P79194 macaca mula
5	55	100.0	638	1	GHR_PIG	P19756 sus scrofa
6	55	100.0	638	1	GHR_RABIT	P19941 oryctolagus
7	55	100.0	638	1	GHR_RAT	P16310 rattus norv
8	55	100.0	650	1	GHR_MOUSE	P16882 mus musculu
9	49	89.1	608	1	GHR_CHICK	Q20992 gallus gall
10	49	89.1	611	1	GHR_COLL	O90375 columba liv
11	42	76.4	1409	1	RPOC_PSEPU	P19176 pseudomonas
12	41	74.5	704	1	SPF2_BOMMO	P20613 bombyx mori
13	40	72.7	1363	1	VRG3_MOUSE	P35917 mus musculu
14	38	69.1	103	1	RPOC_MAIZE	O04438 zea mays (m
15	35	67.3	341	1	MURB_SHEON	O86k85 shewanella
16	37	67.3	1298	1	VRG3_HUMAN	P35916 homo sapien
17	36	65.5	243	1	YQF5_BACSU	P54451 bacillus su
18	36	65.5	316	1	YQ15_CABEL	Q09278 caenorhabdi
19	36	65.5	358	1	Y4PF_RHIN	P55454 rhizobium s
20	36	65.5	694	1	PRE5_YEAST	O08908 saccharomyc
21	35	63.6	514	1	ZRF1_MOUSE	P54103 mus musculu
22	35	63.6	521	1	MTAL_ARTU	P31974 arthrobacte
23	35	63.6	533	1	UGT5_CABEL	Q20086 caenorhabdi
24	35	63.6	568	1	ZRF1_HUMAN	Q99543 homo sapien
25	35	63.6	690	1	CRN1_MOUSE	Q9Cqc1 mus musculu
26	35	63.6	848	1	CRN1_HUMAN	Q9bzj0 homo sapien
27	35	63.6	853	1	CRNB_BOVIN	P23439 bos taurus
28	35	63.6	854	1	CRNB_HUMAN	P35913 homo sapien
29	35	63.6	856	1	CRNB_CANFA	P33726 canis fami
30	35	63.6	856	1	CRNB_MOUSE	P23440 mus musculu
31	34.5	62.7	3707	1	PGBM_MOUSE	Q05793 mus musculu
32	34.5	62.7	4391	1	PGBM_MOUSE	P98160 homo sapien
33	34	61.8	80	1	RUB1_METUA	Q58145 methanococ

```
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CBD2E CRC64;

Query Match 100.0%; Score 55; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 336 DSWVEFIELD 345

RESULT 2
GHR_SHEEP
ID GHR_SHEEP STANDARD; PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1990117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver."
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M82912; AAA73171.1; .
DR PIR; S33339; S33339.
DR HSP; P10912; 1AXT.
DR InterPro; IPR002896; CRIA.
DR InterPro; IPR003961; FN.III.
DR Pfan; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO REC L FL; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 634
FT DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 261 284 POTENTIAL.
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.
FT DISULFID 56 66 BY SIMILARITY.
FT DISULFID 97 108 BY SIMILARITY.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; PFD28B9C23BC1496 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 336 DSWVEFIELD 345

RESULT 3
GHR_HUMAN
ID GHR_HUMAN STANDARD; PRT; 638 AA.
AC P10912;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=88065896; PubMed=2825030;
RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,
RA Hezel W.J., Barnard R., Waters M.J., Wood W.I.;
RT "Growth hormone receptor and serum binding protein: purification,
RT cloning and expression."
RL Nature 330:537-543(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LEU-544.
RX MEDLINE=90046742; PubMed=2813379;
RA Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,
RA Keret R., Rowein P.S., Parks J.S., Larson Z., Wood W.I.;
RT "Characterization of the human growth hormone receptor gene and
RT demonstration of a partial gene deletion in two patients with Laron-
RT type dwarfism."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8083-8087(1989).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=90153957; PubMed=2406245;
RA Fuh G., Mulkerin M.G., Bass S., McFarland N., Brochier M.,
RA Bourrel J.H., Light D.R., Wells J.A.;
RT "The human growth hormone receptor. Secretion from Escherichia coli
RT and disulfide bonding pattern of the extracellular binding domain."
RN J. Biol. Chem. 265:3111-3115(1990).
RN [4]
RP VARIANT LARON DWARFISM SER-114.
RX MEDLINE=89384829; PubMed=2779634;
RA Anselm S., Duquesnoy P., Attree O., Novelli G., Boushina S.,
RA Postelvinay M.-C., Goossens M.;
RT "Laron dwarfism and mutations of the growth hormone-receptor gene."
RN New Engl. J. Med. 321:989-995(1989).
RN [5]
RP VARIANTS LARON DWARFISM.
RX MEDLINE=9378381; PubMed=8504296;
RA Anselm S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
RA Vallet S., Goossens M.;
RT "Spectrum of growth hormone receptor mutations and associated
RT haplotypes in Laron syndrome."
RN Hum. Mol. Genet. 2:355-359(1993).
RN [6]
RP VARIANT LARON DWARFISM HIS-170.
RX MEDLINE=94185645; PubMed=8137822;
```

RA Dusquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R.,
 RA Savage M.O., Preece M.A., Craescu C.T., Blouquit Y., Goossens M.,
 RA Anselm S.;
 RA "A single amino acid substitution in the exoplasmic domain of the
 RT human growth hormone (GH) receptor confers familial GH resistance
 RT (Laron syndrome) with positive GH-binding activity by abolishing
 RT receptor homodimerization.";
 RL EMBO J. 13:1386-1395(1994).
 RN [7]
 RP VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242.
 RX MEDLINE=96013502; PubMed=7565946;
 RA Goddard A.D., Covello R., Luoh S.-M., Clarkson T., Attie K.M.,
 RA Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.M.S.;
 RA "Mutations of the growth hormone receptor in children with idiopathic
 RT short stature.";
 RL New Engl. J. Med. 333:1093-1098(1995).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.
 RX MEDLINE=92196577; PubMed=1549776;
 RA de Vos A.M., Ultsch M., Kossiakoff A.A.;
 RA "Human growth hormone and extracellular domain of its receptor:
 RT crystal structure of the complex.";
 RL Science 255:306-312(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.
 RX MEDLINE=97113023; PubMed=8943276;
 RA Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,
 RA Norstedt G.;
 RT "Crystal structure of an antagonist mutant of human growth hormone,
 RT G120R, in complex with its receptor at 2.9-A resolution.";
 RL J. Biol. Chem. 271:32197-32203(1996).
 RN [10]
 RP VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579.
 RX MEDLINE=99318093; PubMed=10391203;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RA "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 RN [11]
 RP ERRATUM.
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: Defects in GHR are a cause of Laron dwarfism
 CC [MIM:262500]; also known as pituitary dwarfism II (Laron-type
 CC pituitary dwarfism or Laron syndrome (LS)).
 CC -!- DISEASE: Defects in GHR are a cause of idiopathic short stature
 CC [MIM:600946].
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 1.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X06562; CAA29808.1; --
 DR EMBL; M28466; AAA52555.1; --
 DR EMBL; M28458; AAA52555.1; JOINED.
 DR EMBL; M28459; AAA52555.1; JOINED.
 DR EMBL; M28460; AAA52555.1; JOINED.

DR EMBL; M28461; AAA52555.1; JOINED.
 DR EMBL; M28462; AAA52555.1; JOINED.
 DR EMBL; M28463; AAA52555.1; JOINED.
 DR EMBL; M28464; AAA52555.1; JOINED.
 DR EMBL; M28465; AAA52555.1; JOINED.
 DR PIR; A33991; A33991.
 DR PDB; 3HRH; 30-APR-94.
 DR PDB; 1HWG; 19-NOV-97.
 DR PDB; 1WHH; 19-NOV-97.
 DR PDB; 1AXI; 28-JAN-98.
 DR PDB; 1A22; 29-APR-98.
 DR PDB; 1KF9; 20-NOV-02.
 DR Genew; HGNC:4263; GHR.
 DR MIM; 600946; --
 DR MIM; 262500; --
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004903; F:growth hormone receptor activity; TAS.
 DR GO; GO:0007150; P:growth pattern; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;
 KW Dwarfism; Polymorphism; Disease mutation.
 FT SIGNAL 1 18
 FT CHAIN 19 638
 FT DOMAIN 19 264
 FT TRANSMEM 265 288
 FT DOMAIN 289 638
 FT DOMAIN 145 252
 FT DISULFID 56 66
 FT DISULFID 101 112
 FT DISULFID 126 140
 FT CARBOHYD 46 46
 FT CARBOHYD 115 115
 FT CARBOHYD 156 156
 FT CARBOHYD 161 161
 FT CARBOHYD 200 200
 FT VARIANT 62 62
 FT VARIANT 89 89
 FT VARIANT 114 114
 FT VARIANT 143 143
 FT VARIANT 162 162
 FT VARIANT 170 170
 FT VARIANT 179 179
 FT VARIANT 179 179
 FT VARIANT 229 229
 FT VARIANT 229 229
 FT VARIANT 242 242
 FT VARIANT 440 440
 FT VARIANT 495 495
 FT VARIANT 544 544
 FT
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT E -> K (in idiopathic short stature).
 FT /FTId=VAR_002708
 FT R -> K (in Laron dwarfism).
 FT /FTId=VAR_002709.
 FT F -> S (in Laron dwarfism).
 FT /FTId=VAR_002710.
 FT V -> A (in Laron dwarfism).
 FT /FTId=VAR_002711.
 FT V -> D (in Laron dwarfism).
 FT /FTId=VAR_002712.
 FT D -> H (in Laron dwarfism; abolish
 FT receptor homodimerization).
 FT /FTId=VAR_002713.
 FT R -> C (in Laron dwarfism and idiopathic
 FT short stature).
 FT /FTId=VAR_002714.
 FT R -> H (in dBSNP:6181).
 FT /FTId=VAR_013937.
 FT R -> G (in Laron dwarfism).
 FT /FTId=VAR_02715.
 FT R -> H (in dBSNP:6177).
 FT /FTId=VAR_013938.
 FT E -> D (in idiopathic short stature).
 FT /FTId=VAR_002716.
 FT C -> F (in dBSNP:6182).
 FT /FTId=VAR_013939.
 FT P -> T (in dBSNP:6183).
 FT /FTId=VAR_013940.
 FT I -> L (in dBSNP:6180).
 FT /FTId=VAR_013941.

Query Match

100.0%; Score 55; DB 1; Length 638;

GHR_RABIT STANDARD; PRT; 638 AA.

AC P19941;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
 GN GHR.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=8805896; PubMed=2825030;
 RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Henzel W.J., Barnard R., Waters M.J., Wood W.I.;
 RT "Growth hormone receptor and serum binding protein: purification, cloning and expression."
 RL Nature 330:537-543(1987).
 CC -1- FUNCTION: This is a receptor for pituitary gland growth hormone.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF015252; AAB67613.1; -.
 DR PIR; S08544; B28176.
 DR HSP; P10912; 1A22.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.
 FT DOMAIN 19 264 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 265 288 POTENTIAL.
 FT DOMAIN 289 638 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 145 252 FIBRONECTIN TYPE-III.
 FT DISULFID 56 66 BY SIMILARITY.
 FT DISULFID 101 112 BY SIMILARITY.
 FT DISULFID 126 140 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 638 AA; 71076 MW; E05CCE1D7294624C CRC64;
 Query Match 100.0%; Score 55; DB 1; Length 638;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSWVEFIELD 10
 Db 340 DSWVEFIELD 349

RESULT 7
 GHR_RAT

GHR_RAT STANDARD; PRT; 638 AA.

AC P16310;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).
 GN GHR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89255563; PubMed=2722883;
 RA Mathews L.S., Enberg B., Norsted G.;
 RT "Regulation of rat growth hormone receptor gene expression."
 RL J. Biol. Chem. 264:9905-9910(1989).
 CC [2]
 CC SEQUENCE FROM N.A.
 RX MEDLINE=9006741; PubMed=2792761;
 RA Baumbach W.R., Horner D.L., Logan J.S.;
 RT "The growth hormone-binding protein in rat serum is an alternatively spliced form of the rat growth hormone receptor."
 RL Genes Dev. 3:1199-1205(1989).
 CC -1- FUNCTION: This is a receptor for pituitary gland growth hormone.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 DR EMBL; J04811; AAA41219.1; -.
 DR PIR; A32985; A33505.
 DR HSP; P10912; 1A22.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.
 FT DOMAIN 19 265 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 266 289 POTENTIAL.
 FT DOMAIN 290 638 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 145 252 FIBRONECTIN TYPE-III.
 FT DISULFID 56 66 BY SIMILARITY.
 FT DISULFID 101 112 BY SIMILARITY.
 FT DISULFID 126 140 BY SIMILARITY.
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 638 AA; 71236 MW; 0D8E9AF759A21A3B CRC64;
 Query Match 100.0%; Score 55; DB 1; Length 638;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSWVEFIELD 10
 Db 341 DSWVEFIELD 350

RESULT 8

GHR_MOUSE
 ID GHR_MOUSE STANDARD; PRT; 650 AA.
 AC P16882; P16590; Q9R264;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Growth hormone receptor precursor (GH receptor) (GH binding protein)
 DE (GHRP) (Serum binding protein).
 GN GHR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=9295449; PubMed=2739661;
 RT Smith W.C., Kuniyoshi J., Talamantes F.;
 RT "Mouse serum growth hormone (GH) binding protein has GH receptor
 RT extracellular and substituted transmembrane domains.";
 RL Mol. Endocrinol. 3:984-990(1989).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=Swiss Webster, and DBA/2J;
 RX MEDLINE=9367316; PubMed=10425445;
 RA Moffat J.G., Edens A., Talamantes F.;
 RT "Structure and expression of the mouse growth hormone receptor/growth
 RT hormone binding protein gene.";
 RL J. Mol. Endocrinol. 23:333-44(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=Swiss Webster, and DBA/2J;
 RX MEDLINE=95080157; PubMed=7988474;
 RA Edens A., Southard J.N., Talamantes F.;
 RT "Mouse growth hormone receptor/binding protein and growth hormone
 RT receptor transcripts are produced from a single gene by alternative
 RT splicing.";
 RL Endocrinology 135:2802-2805(1994).
 RN [4]
 RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6;
 RX MEDLINE=95201642; PubMed=7894338;
 RA Zhou Y., He L., Koppchick J.J.;
 RT "An exon encoding the mouse growth hormone binding protein (mGHBP)
 RT carboxy terminus is located between exon 7 and 8 of the mouse growth
 RT hormone receptor gene.";
 RL Receptor 4:223-227(1994).
 RN [5]
 RP REVISIONS.
 RA Zhou Y., He L., Koppchick J.J.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 25-41.
 RX MEDLINE=88288223; PubMed=3398846;
 RA Smith W.C., Colosi P., Talamantes F.;
 RT "Isolation of two molecular weight variants of the mouse growth
 RT hormone receptor.";
 RL Mol. Endocrinol. 2:108-116(1988).
 CC -1- FUNCTION: Isoform 1 is a receptor for pituitary gland growth
 CC hormone. Isoform 2 is a serum growth hormone binding protein that
 CC may play an important role in regulating the effective serum
 CC concentration of gh.
 CC -1- SUBUNIT: Isoform 1 is a homodimer.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC Secreted (isoform 2).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=HWM GHR;
 CC IsoId=P16882-1; Sequence=Displayed;
 CC Name=2; Synonyms=LWM GHR;
 CC IsoId=P16882-2; Sequence=VSP 001716, VSP 001717;
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.

Subfamily 1.
 -1- SIMILARITY: Contains 1 fibronectin type III domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M33324; AAA37690.1; ALT SEQ.
 DR EMBL; M31680; AAA37689.1; ALT SEQ.
 DR EMBL; AF120489; AAD32556.1;
 DR EMBL; AF120481; AAD32556.1; JOINED.
 DR EMBL; AF120482; AAD32556.1; JOINED.
 DR EMBL; AF120483; AAD32556.1; JOINED.
 DR EMBL; AF120484; AAD32556.1; JOINED.
 DR EMBL; AF120485; AAD32556.1; JOINED.
 DR EMBL; AF120486; AAD32556.1; JOINED.
 DR EMBL; AF120487; AAD32556.1; JOINED.
 DR EMBL; AF120488; AAD32556.1; JOINED.
 DR EMBL; AF120487; AAD32555.1;
 DR EMBL; AF120481; AAD32555.1; JOINED.
 DR EMBL; AF120482; AAD32555.1; JOINED.
 DR EMBL; AF120483; AAD32555.1; JOINED.
 DR EMBL; AF120484; AAD32555.1; JOINED.
 DR EMBL; AF120485; AAD32555.1; JOINED.
 DR EMBL; AF120486; AAD32555.1; JOINED.
 DR EMBL; U49266; AAK62802.1;
 DR EMBL; U49268; AAK62802.1; JOINED.
 DR EMBL; U43933; AAK62802.1; JOINED.
 DR HGSP; P10912; IA22.
 DR MGD; MGI:95708; Ghr.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003528; Hemtopoptn_L_Fl.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO REC L Fl; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 650 GROWTH HORMONE RECEPTOR.
 FT DOMAIN 25 273 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 274 297 POTENTIAL.
 FT DOMAIN 298 650 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 153 260 FIBRONECTIN TYPE-III.
 FT DISULFID 56 66 BY SIMILARITY.
 FT DISULFID 109 120 BY SIMILARITY.
 FT DISULFID 134 148 BY SIMILARITY.
 FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 271 296 DIQPPWFLIIIFGIFGVAVMLFVVIF -> GIKSNSQHPHQ
 FT EIDNHYHQIRRH (in isoform 2).
 FT VARSPLIC 297 650 Missing (in isoform 2).
 FT VARSPLIC 297 650 Missing (in isoform 2).
 FT CONFLICT 25 25 T -> A (IN REF. 6).
 FT CONFLICT 162 162 G -> A (IN REF. 3 AND 4).
 FT CONFLICT 325 325 E -> G (IN REF. 2).
 FT CONFLICT 423 423 R -> A (IN REF. 2).
 SQ SEQUENCE 650 AA; 72783 MW; 95653380CAF0B931 CRC64;
 Query Match 100.0%; Score 55; DB 1; Length 650;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DSWVERIELD 10
 |||||
 Db 349 DSWVERIELD 358

```

RESULT 9
GHR_CHICK
ID GHR_CHICK STANDARD; PRT; 608 AA.
AC Q02092;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91243665; PubMed=2036984;
RA Burnside J., Liou S.S., Cogburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens.";
RL Endocrinology 128:3183-3192(1991).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Broad specificity.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M74057; AAA48781.1; -.
DR F01; S32823; S32823.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CRI1A.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 608 GROWTH HORMONE RECEPTOR.
FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 261 POTENTIAL.
FT DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 72 83 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 89.1%; Score 49; DB 1; Length 608;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
DB 313 DLWVEFIELD 322

```

```

RESULT 10
GHR_COLLI
ID GHR_COLLI STANDARD; PRT; 611 AA.
AC Q90375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U20353; AAA84745.1; -.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CRI1A.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.
FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 264 POTENTIAL.
FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 226 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 100 114 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 611 AA; 68851 MW; C48750BF9E4EBDA CRC64;

Query Match 89.1%; Score 49; DB 1; Length 611;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
DB 316 DLWVEFIELD 325

```

RESULT 11

```

RPOC_PSEPU
ID _RPOC_PSEPU STANDARD; PRT; 1409 AA.
AC P19176;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Danilovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.I., Monastyrskaya G.S., Sverdlov E.D.;
RT "Nucleotide sequence of the rpoC gene coding for the beta'-subunit of
RT RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 303:241-245 (1988).
RN [2]
RP SEQUENCE OF 1-497 FROM N.A.
RX MEDLINE=89117617; PubMed=3219133;
RA Borodin A.M., Danilovich A.V., Chernov I.P., Azhikina T.L.,
RA Rostapshov V.M., Monastyrskaya G.S.;
RT "Genes coding for RNA polymerase in bacteria. III. The use of
RT modified Sanger's method for sequencing the C-terminal region of rpoB
RT gene, N-terminal region of rpoC gene and intercistron region of rpoB
RT polymerase in Pseudomonas putida.";
RL Bioorg. Khim. 14:1179-1182 (1988).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}[N].
CC -!- SUBUNIT: The enzyme consists of the sigma chain and the core
CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
CC beta' chain.
CC -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X16538; CAA34538.1; -.
CC EMBL; M38319; AAA25987.1; -.
CC PIR; JN0420; JN0420.
CC HSPG; Q9KWU6; 1HQW.
CC InterPro; IPR007072; RNA_pol_A.
CC InterPro; IPR007080; RNA_pol_Rpb1_1.
CC InterPro; IPR007066; RNA_pol_Rpb1_3.
CC InterPro; IPR007083; RNA_pol_Rpb1_4.
CC InterPro; IPR007081; RNA_pol_Rpb1_5.
CC InterPro; IPR006592; RNA_pol_N.
CC Pfam; PF04997; RNA_pol_Rpb1_1.
CC Pfam; PF00623; RNA_pol_Rpb1_2.
CC Pfam; PF04983; RNA_pol_Rpb1_3.
CC Pfam; PF05000; RNA_pol_Rpb1_4.
CC Pfam; PF04998; RNA_pol_Rpb1_5.
CC SMART; SM00663; RPOA_N; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription.
FT CONFLICT 2 2 P -> L (IN REF. 2).
FT CONFLICT 17 17 N -> I (IN REF. 2).
FT CONFLICT 89 89 L -> V (IN REF. 2).
FT CONFLICT 203 203 I -> T (IN REF. 2).
FT CONFLICT 328 328 I -> T (IN REF. 2).
FT CONFLICT 335 335 L -> S (IN REF. 2).
FT CONFLICT 348 348 L -> R (IN REF. 2).
FT CONFLICT 482 482 P -> L (IN REF. 2).

FT CONFLICT 484 484 T -> I (IN REF. 2).
SQ SEQUENCE 1409 AA; 154544 MW; C5662109D3BE3D81 CRC64;

Query Match 76.4%; Score 42; DB 1; Length 1409;
Best Local Similarity 70.0%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
: |||||:
DB 877 EQWVEFIELDN 886

RESULT 12
SSP2_BOMMO STANDARD; PRT; 704 AA.
ID _SSP2_BOMMO
AC P20613;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Sex-specific storage-protein 2 precursor.
GN SP2.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
CX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201839; PubMed=2544581;
RA Fujii T., Sakurai H., Izumi S., Tomino S.;
RT "Structure of the gene for the arylphorin-type storage protein SP 2
RT of Bombyx mori.";
RL J. Biol. Chem. 264:11020-11025 (1989).
CC -!- FUNCTION: Larval storage protein (LSP) which may serve as a store
CC of amino acids for synthesis of adult proteins.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Fat body.
CC -!- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24370; AAA27848.1; -.
CC EMBL; M24371; AAA27848.1; JOINED.
CC PIR; A34287; A34287.
CC HSPG; P04253; 1OXY.
CC InterPro; IPR008922; Di-copper centre.
CC InterPro; IPR00896; Hemocyanin.
CC InterPro; IPR005203; hemocyanin_C.
CC InterPro; IPR005204; hemocyanin_N.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00372; hemocyanin_1.
CC Pfam; PF03723; hemocyanin_C.
CC Pfam; PF03722; hemocyanin_N.
CC PRINTS; PS00187; HAEMOCYANIN.
CC PROSITE; PS00209; HEMOCYANIN_1.
CC PROSITE; PS00210; HEMOCYANIN_2.
CC Signal; Storage protein; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 704 SEX-SPECIFIC STORAGE-PROTEIN 2.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 704 AA; 83466 MW; 365E7DFB707137EB CRC64;

Query Match 74.5%; Score 41; DB 1; Length 704;
Best Local Similarity 60.0%; Pred. No. 6.4;

```

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10
Db 544 DNMMKFFELD 553

RESULT 13
VGR3 MOUSE
ID_VGR3 MOUSE STANDARD; PRT; 1363 AA.

AC P35917;
DT 01-JUN-1994 (Rel. 29, last sequence update)
DT 01-JUN-1994 (Rel. 29, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
DE (VEGFR-3) (tyrosine-protein kinase receptor FLT4).
GN FLT4 OR FLT-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=9330572; PubMed=8393164;
RA Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,
RA Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.;
RT "Molecular cloning of murine FLT and FLT4";
RL Oncogene 8:2293-2298(1993).
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE
CC ACTIVITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN
CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.
CC CSF-1/PDGF receptor subfamily.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; L07296; AAA00077.1; -.
DR PIR; I58375; I58375.
DR HSSP; P11362; 1FGK.
DR MGD; MGI:95561; Flt4.
DR GO; GO:0005515; F-protein binding; IPI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR001824; RecepttyrkinsIII.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF00047; Ig; 5.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 2.
DR SMART; SM00408; IGC2; 2.
DR SMART; SM00219; TykKc; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
DR PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.
KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;
KW Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 1363 VASCULAR ENDOTHELIAL GROWTH FACTOR
FT RECEPTOR 3.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM
FT DOMAIN 25 775
FT TRANSMEM 776 797
FT DOMAIN 798 1363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 118 IG-LIKE C2-TYPE 1.
FT DOMAIN 151 213 IG-LIKE C2-TYPE 2.
FT DOMAIN 230 326 IG-LIKE C2-TYPE 3.
FT DOMAIN 331 415 IG-LIKE C2-TYPE 4.
FT DOMAIN 422 552 IG-LIKE C2-TYPE 5.
FT DOMAIN 555 671 IG-LIKE C2-TYPE 6.
FT DOMAIN 678 764 IG-LIKE C2-TYPE 7.
FT DOMAIN 845 1173 PROTEIN KINASE.
FT NP_BIND 851 859 ATP (BY SIMILARITY).
FT BINDING 879 879 ATP (BY SIMILARITY).
FT ACT_SITE 1037 1037 BY SIMILARITY.
FT DISULFID 51 111 POTENTIAL.
FT DISULFID 158 206 POTENTIAL.
FT DISULFID 252 310 POTENTIAL.
FT DISULFID 445 534 POTENTIAL.
FT DISULFID 578 653 POTENTIAL.
FT DISULFID 699 751 POTENTIAL.
FT MOD_RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 690 690 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1363 AA; 153015 MW; F1BF8A2BDEF99BE9 CRC64;

Query Match 72.7%; Score 40; DB 1; Length 1363;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVERIE 8
Db 505 DSWTEFVE 512

RESULT 14
SR09 MAIZE
ID_SR09 MAIZE STANDARD; PRT; 103 AA.
AC O0438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal recognition particle 9 kDa protein (SRP9).
GN SRP9.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W64A2;
RA Bui N., Wolff N., Strub K.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Signal-recognition-particle assembly has a crucial role
CC in targeting secretory proteins to the rough endoplasmic reticulum
CC membrane. SRP9 together with SRP14 and the Alu portion of the SRP
CC RNA, constitutes the elongation arrest domain of SRP. The complex
CC of SRP9 and SRP14 is required for SRP RNA binding (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the SRP9 family.

```
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y10117; CAA71203.1; -.
DR PIR; T03951; T03951.
DR HSSP; P49662; 1914.
DR InterPro; IPR008832; SRP9.
DR InterPro; IPR009018; SRP9/14.
DR Pfam; PF05486; SRP9; 1.
KW Signal recognition particle; RNA-binding.
SQ SEQUENCE 103 AA; 12077 MW; B6EFA49DA77C13BE CRC64;
Query Match 69.1%; Score 38; DB 1; Length 103;
Best Local Similarity 75.0%; Pred. No. 3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DSWVEFTIE 8
Db |||||:|
5 DSWEEFVE 12
RESULT 15
MURB SHEON STANDARD; PRT; 341 AA.
ID MURB SHEON
AC Q8EK85;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE acetylmuramate dehydrogenase).
DE MURB OR S00213.
GN Shewanella oneidensis.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vanathevan J., Weidman J., Imbraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., C.M.;
RA Feidblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -!- FUNCTION: Cell wall formation (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC -!- COFACTOR: FAD (By similarity).
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murB family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE015471; AAN53298.1; -.

```

```
DR TIGR; S00213; -.
DR HAMAP; MF 00037; -.
DR InterPro; IPR003170; MurB.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD_binding_4; 1.
DR Pfam; PF02873; MurB_C; 1.
DR TIGRFAMs; TIGR00179; murB; 1.
KW Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
KW Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 341 AA; 37278 MW; FAE630BA722A3073 CRC64;
Query Match 67.3%; Score 37; DB 1; Length 341;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 WVEFIELD 10
Db |||||:|
137 WVEYLDLD 144
Search completed: June 9, 2004, 15:49:05
Job time : 7.2973 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 33.5135 seconds
(without alignments)
94.147 Million cell updates/sec

Title: US-09-660-302D-3
Perfect score: 55
Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_ivirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	100.0	101	6 Q863N9	arctonyx co
2	55	100.0	105	6 Q863Q6	lontra cana
3	55	100.0	105	6 Q863P4	eira barbar
4	55	100.0	106	6 Q863Q3	lutra lutra
5	55	100.0	106	6 Q863Q2	lutra macul
6	55	100.0	107	6 Q863Q9	acnyx capen
7	55	100.0	107	6 Q863Q8	amblyonx ci
8	55	100.0	107	6 Q863Q7	enhydra lut
9	55	100.0	107	6 Q863Q5	lontra feli
10	55	100.0	107	6 Q863Q4	lontra long
11	55	100.0	107	6 Q863Q1	pteronura b
12	55	100.0	107	6 Q863Q0	mustela erm
13	55	100.0	107	6 Q863P9	mustela fire
14	55	100.0	107	6 Q863P8	mustela vis
15	55	100.0	107	6 Q863P7	martes amer
16	55	100.0	107	6 Q863P6	martes penn

17	55	100.0	107	6 Q863P5	gulo gulo (
18	55	100.0	107	6 Q863P2	ictonyx str
19	55	100.0	107	6 Q863P1	meles meles
20	55	100.0	107	6 Q863P0	taxidea tax
21	55	100.0	107	6 Q863N8	melogale mo
22	55	100.0	107	6 Q863N7	bassariscus
23	55	100.0	107	6 Q863N6	procyon lot
24	55	100.0	130	11 Q99M17	meriones un
25	55	100.0	233	6 Q95MM1	ochotona pr
26	55	100.0	238	11 Q924F8	perognathus
27	55	100.0	293	6 Q8MJM2	elephantulu
28	55	100.0	294	6 Q95ML9	syllilagus
29	55	100.0	294	6 Q8MJL9	ursus ameri
30	55	100.0	295	6 Q95ML8	tupaia bela
31	55	100.0	295	11 Q80Z48	Q924F8
32	55	100.0	296	11 Q924F4	ctenomys st
33	55	100.0	296	11 Q924F1	hystrix afr
34	55	100.0	296	11 Q924E8	chinchilla
35	55	100.0	296	11 Q924F2	proechimys
36	55	100.0	296	11 Q924F3	thryonomys
37	55	100.0	296	11 Q924B9	Q924F3
38	55	100.0	296	11 Q924F0	heterocepha
39	55	100.0	296	11 Q80Z55	dinomys bra
40	55	100.0	296	11 Q80Z54	erethizon d
41	55	100.0	296	11 Q80Z53	aconaemys p
42	55	100.0	296	11 Q80Z52	octodon bri
43	55	100.0	296	11 Q80Z51	octodontomy
44	55	100.0	296	11 Q80Z49	spalacopus
45	55	100.0	296	11 Q80Z47	typanoctom
					aconaemys f

ALIGNMENTS

RESULT 1

ID Q863N9 PRELIMINARY; PRT; 101 AA.
AC Q863N9; (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Arctonyx collaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;
OC Arctonyx.
OX NCBI_TaxID=139309;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498204; AAP19695.1; -
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 101
SQ SEQUENCE 101 AA; 11428 MW; AD696CB6E0E8D7AC CRC64;

Query Match 100.0%; Score 55; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
|||
Db 25 DSWVEFIELD 34
|||

RESULT 2

ID Q863Q6 PRELIMINARY; PRT; 105 AA.

```

AC Q86306;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra canadensis (River otter) (Lontra canadensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lontra.
OX NCBI_TaxID=76717;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498197; AAPI9678.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 105
SQ SEQUENCE 105 AA; 11852 MW; F07A7052451EB8E7 CRC64;

Query Match 100.0%; Score 55; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 29 DSWVEFIELD 38

RESULT 3
Q863P4
ID Q863P4 PRELIMINARY; PRT; 105 AA.
AC Q863P4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Eira barbara (Tayra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Eira.
OX NCBI_TaxID=204263;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498199; AAPI9690.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 105
SQ SEQUENCE 105 AA; 11879 MW; F6F6445250DB79BF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 29 DSWVEFIELD 38

RESULT 4
Q863Q3
ID Q863Q3 PRELIMINARY; PRT; 106 AA.
AC Q863Q3;

```

```

DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra lutra (European river otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lontra.
OX NCBI_TaxID=9657;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498190; AAPI9681.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 12006 MW; EFB0C6D8793AE9FF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 30 DSWVEFIELD 39

RESULT 5
Q863Q2
ID Q863Q2 PRELIMINARY; PRT; 106 AA.
AC Q863Q2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra maculicollis (Spotted necked otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lutra.
OX NCBI_TaxID=76719;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498191; AAPI9682.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 12003 MW; EFB0DDAEA24C29FF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 30 DSWVEFIELD 39

RESULT 6
Q863Q9
ID Q863Q9 PRELIMINARY; PRT; 107 AA.
AC Q863Q9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)

```

```

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Anonyx capensis (Cape clawless otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Anonyx.
OX NCBI_TaxID=76722;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498184; AAP19675.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12101 MW; 7F3D579D3C26011B CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 7
Q863Q8 ID Q863Q8 PRELIMINARY; PRT; 107 AA.
AC Q863Q8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Amblyonyx cinereus (Asian small-clawed otter) (Anonyx cinereus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Amblyonyx.
OX NCBI_TaxID=55043;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498185; AAP19676.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 8
Q863Q7 ID Q863Q7 PRELIMINARY; PRT; 107 AA.
AC Q863Q7;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

```

```

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Euhadra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Euhadra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498186; AAP19677.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12151 MW; 84DD579D3C2EA9FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 9
Q863Q5 ID Q863Q5 PRELIMINARY; PRT; 107 AA.
AC Q863Q5;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra felina (Sea cat) (Lutra felina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lontra.
OX NCBI_TaxID=76718;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498188; AAP19679.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 10
Q863Q4 ID Q863Q4 PRELIMINARY; PRT; 107 AA.
AC Q863Q4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

```

```

DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=71113;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498189; AAP19680.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12166 MW; 9113E146451EA8BB CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 11
Q863Q1 PRELIMINARY; PRT; 107 AA.
AC Q863Q1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Pteronura brasiliensis (Giant otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Pteronura.
OX NCBI_TaxID=9672;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498192; AAP19683.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12137 MW; 96DBCA309E7789FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 12
Q863Q0 PRELIMINARY; PRT; 107 AA.
AC Q863Q0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

```

```

GN GHR.
OS Mustela erminea (Ermine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=36723;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498193; AAP19684.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 13
Q863P9 PRELIMINARY; PRT; 107 AA.
AC Q863P9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Mustela frenata (Long-tailed weasel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=55048;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498194; AAP19685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 14
Q863P8 PRELIMINARY; PRT; 107 AA.
AC Q863P8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

```

```

OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1];
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498195; AAP19686.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12149 MW; 96CCE146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10
Db 31 DSWVERFIELD 40

RESULT 15
Q863P7
ID Q863P7 PRELIMINARY; PRT; 107 AA.
AC Q863P7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Martes americana (American marten).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Martes.
OX NCBI_TaxID=9660;
RN [1];
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498196; AAP19687.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12172 MW; 96DBD14658B649FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10
Db 31 DSWVERFIELD 40

Search completed: June 9, 2004, 15:51:22
Job time : 33.5135 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 35 seconds
(without alignments)
56.510 Million cell updates/sec

Title: US-09-660-302D-7

Perfect score: 43

Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: Geneseqp1990s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DB ID	Description
1	43	100.0	7	2	AAY32791	Aay32791 Proteolyt
2	38	88.4	9	5	ABG94867	Abg94867 Human hGH
3	38	88.4	9	7	AD82293	Ad82293 Plasmid p
4	38	88.4	33	2	AAR22456	Aar22456 Plasmid p
5	38	88.4	246	2	AAR56389	Aar56389 Human gro
6	38	88.4	249	2	AAR06867	Aar06867 Hormone b
7	38	88.4	269	2	AAR05045	Aar05045 Soluble h
8	38	88.4	269	2	AAM10426	Aaw10426 Human som
9	38	88.4	269	2	AAY31767	Aay31767 Human sol
10	38	88.4	269	2	AAY82802	Aaw82802 Human sol
11	38	88.4	269	3	AAY78429	Aay78429 Soluble p
12	38	88.4	269	7	AD82252	Ad82252 Plasmid p
13	38	88.4	315	5	Aau75499	Aau75499 Human fus
14	38	88.4	340	5	Aau75496	Aau75496 Human fus
15	38	88.4	637	1	AAP92108	Aap92108 Human gro
16	38	88.4	638	1	AAP81326	Aap81326 Human gro
17	38	88.4	638	2	AAW33394	Aaw33394 Human gro
18	38	88.4	638	7	ADDA5067	Add5067 Human pro
19	38	88.4	648	7	ADDA5063	Add5063 Human pro
20	38	88.4	648	4	ABBI1437	Abbi1437 Human gro
21	37	86.0	460	6	ABU33279	Abu33279 Protein e
22	36	83.7	84	2	AAY30432	Aay30432 Mature ne
23	36	83.7	84	3	ABBI5317	Aabi5317 A. caninu
24	36	83.7	91	2	AAR91701	Aar91701 AcanAPC2.
25	36	83.7	91	2	AAY30393	Aay30393 Nematode

ALIGNMENTS

RESULT 1

AAY32791
ID AAY32791 standard; peptide; 7 AA.

XX AC AAY32791;

XX DT 09-NOV-1999 (first entry)

XX DE Proteolytic cleavage signal site used in inhibiting receptor proteolysis.

KW Signal transduction; proteolytic cleavage; cleavage signal site;

KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;

KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS;

KW Growth hormone deficiency.

XX OS Mammalia.

XX OS EP943624-A1.

XX PN 22-SEP-1999.

XX PD 12-MAR-1998; 98EP-00200799.

XX PR 12-MAR-1998; 98EP-00200799.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

XX Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

XX Claim 15; Page 27; 36pp; English.

XX This sequence is a cleavage signal site. This site is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The inhibitor is derived from or competes with an amino acid sequence around this proteolytic cleavage signal. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and during neuromuscular disease

XX Sequence 7 AA;

Query Match 100.0%; Score 43; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 |||||
 Db 1 CEEDFYR 7

RESULT 2
 ABG94867
 ID ABG94867 standard; peptide; 9 AA.
 XX AC ABG94867;
 XX DT 03-DEC-2002 (first entry)
 XX DE Human hGH binding protein carboxy terminus from pbGhr (1-246).
 XX KW Growth hormone; placental lactogen; prolactin; active domain; hGH; human;
 KW structure-function relationship; p01446; somatogenic receptor;
 KW segment-substituted polypeptide; hGH binding protein; mutant; mutein.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN US6428954-B1.
 XX PD 06-AUG-2002.
 XX PF 06-JUN-1995; 95US-00483039.
 XX PR 28-OCT-1988; 88US-00264611.
 XX PR 26-OCT-1989; 89US-00428066.
 XX PR 27-APR-1992; 92US-00875204.
 XX PR 13-OCT-1992; 92US-00960227.
 XX PR 02-FEB-1994; 94US-00190723.
 XX PA (GETH) GENENTECH INC.
 XX PI Wells JA, Cunningham BC;
 XX WPI; 2002-696875/75.
 XX N-PSDB; ABS73022.

Identifying active domains within cloned polypeptides of known amino acid sequence by substituting analog segments into the parent polypeptide is useful to determine the relationship between structure and function.

Example 3; Col 31-32; 86pp; English.

The invention relates to identifying an unknown active domain in a region of known amino acid sequence in a parent polypeptide e.g. human growth hormone (hGH) which has been cloned and has a pre-identified biological activity, where the active domain interacts with a target when the parent polypeptide is in its native-folded form and the interaction is responsible for the biological activity comprising: (a) comparing the amino acid sequence or polypeptide structure in the region of known amino acid sequence of hGH with the amino acid sequence of an analogue polypeptide (e.g. prolactin, placental lactogen or porcine growth hormone) which has at least 15% homology with hGH alpha-carbon coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates for about 60% of the analogue sequence, where any interaction of the analogue with the target is different from target interaction with hGH; (b) substituting DNA encoding an analogous polypeptide segment from the analogue into DNA encoding the full length hGH, and expressing a segment-substituted polypeptide; (c) contacting the segment-substituted polypeptide with the target to determine interaction; (d) repeating steps (b) and (c) with a second analogous polypeptide segment; and (e) comparing the difference between activity of the first and second segment-substituted polypeptides as an indication of the location of the unknown

CC active domain in hGH. The method is useful for determining the
 CC relationship between structure and function of known polypeptide
 CC sequences. The present sequence shows a mutated part of an hGH binding
 CC protein, a target polypeptide for hGH used to test the binding of
 CC substitution mutants in the method of the invention
 XX
 SQ Sequence 9 AA;

Query Match 88.4%; Score 38; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
 |||||
 Db 4 CEEDFY 9

RESULT 3
 ADE82293
 ID ADE82293 standard; peptide; 9 AA.
 XX AC ADE82293;
 XX DT 29-JAN-2004 (first entry)
 XX DE plasmid phGhr (1-246) carboxy peptide fragment.
 XX KW human growth hormone; hGH; variant; somatogenic receptor.
 XX OS Synthetic.
 XX PN US6451561-B1.
 XX PD 17-SEP-2002.
 XX PF 07-JUN-1995; 95US-00486474.
 XX PR 28-OCT-1988; 88US-00264611.
 XX PR 26-OCT-1989; 89US-00428066.
 XX PR 27-APR-1992; 92US-00875204.
 XX PR 13-OCT-1992; 92US-00960227.
 XX PR 02-FEB-1994; 94US-00190723.
 XX PA (GETH) GENENTECH INC.
 XX PI Wells JA, Cunningham BC;
 XX WPI; 2003-101735/09.
 XX N-PSDB; ADE82294.

Forming human growth hormone (hGH) variants by substitution mutation so that the variant binds to a target for hGH, e.g. hGH receptors or human prolactin receptors with affinity different from that of wild-type hGH.

Example 3; Col 31-32; 87pp; English.

This invention describes a method for generating a novel human growth hormone (hGH) variant that binds to a target for hGH with an affinity different from affinity of wild type hGH for the target. Human growth hormone (hGH) has a positive binding activity with the target receptor, the somatogenic receptor. The human prolactin (hPRL), human placental lactogen (hPL) and porcine growth hormone (pGH) analogues, however, have a greatly reduced activity with that target. Six segment-substituted growth hormones were formed by substituting selected amino acid segments of hGH with an analogous amino acid segment from the analogue. Each of these selected segments are different and were chosen to probe either the entire amino acid sequence of the hGH molecule or those regions which are expected to contain the active domains. This sequence represents a fragment of plasmid phGhr used in the generation of hGH binding protein constructions.

Sequence 9 AA;

Query Match 88.4%; Score 38; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
 Db 4 CEEDFY 9

RESULT 4
 AAR22456
 ID AAR22456 standard; protein; 33 AA.

XX AC AAR22456;
 XX DT 09-SEP-1992 (first entry)
 XX DE Plasmid pBSR8-3 encoded polypeptide.
 XX KW Recombinant; plasmid pAcYmHGR; hGHR binding region;
 XX KW human growth hormone.
 XX OS Synthetic.
 XX PN JF04063594-A.
 XX PD 28-FEB-1992.
 XX PF 03-JUL-1990; 90JP-00176630.
 XX PR 03-JUL-1990; 90JP-00176630.
 XX PA (TANP-) TANPAKU KAGAKU KENK.
 XX DR WPI; 1992-120154/15.
 XX DR N-PSDB; AAQ23311.

XX PT New recombinant plasmid and Baculovirus having specific DNA fragment -
 XX PT used for prepn. of hormone binding region protein of human growth hormone
 XX PT receptor.
 XX PS Example; Fig 2; 11pp; Japanese.

XX CC The sequence is that encoded by a fragment of the plasmid pBSR8-3 which
 CC is used in the construction of plasmid pAcYmHGR. pAcYmHGR contains a
 CC DNA fragment encoding the binding region of human growth hormone receptor
 CC (hGHR) under control of a Baculovirus gene expression system. This can be
 CC used to transform insect cells to produce a more natural protein than is
 CC obtd. with E.coli and in larger amts. See also AAR22457-R22459
 XX SQ Sequence 33 AA;

Query Match 88.4%; Score 38; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
 Db 28 CEEDFY 33

RESULT 5
 AAR56389
 ID AAR56389 standard; protein; 246 AA.

XX AC AAR56389;
 XX DT 01-MAR-1995 (first entry)
 XX DE Human growth hormone receptor C-domain.

XX KW Human growth hormone receptor; hGHR; C-domain; CD; hGHR-CD;
 KW extracellular; enhancement; Met130Q-238Q; GS129V-238Q.

XX OS Homo sapiens.
 XX PN JF06172394-A.
 XX PD 21-JUN-1994.
 XX PF 10-DEC-1992; 92JP-00330361.
 XX PR 10-DEC-1992; 92JP-00330361.
 XX PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
 XX DR WPI; 1994-238767/29.

XX PT Extracellular C-domain protein of growth hormone receptor (hGHR-CD) - is
 PT used to enhance growth hormone function.
 XX PS Disclosure; Page 9-10; 16pp; Japanese.

XX CC The extracellular C-domain of hGHR is used to enhance growth hormone
 CC function. Two forms, Met130Q-238Q (AAQ66550) and GS129V-238Q (AAQ66553)
 CC are given. Primers for the isolation of extracellular hGHR-CD are given
 CC in AAQ66551-52 and AAQ66554-55

XX SQ Sequence 246 AA;

Query Match 88.4%; Score 38; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
 Db 241 CEEDFY 246

RESULT 6
 AAR06867
 ID AAR06867 standard; protein; 249 AA.

XX AC AAR06867;
 XX DT 16-JAN-1991 (first entry)
 XX DE Hormone binding region of human growth hormone receptor.
 XX KW hGHR.

XX OS Synthetic.

XX PN JF02200186-A.

XX PD 08-AUG-1990.

XX PF 30-JAN-1989; 89JP-00020182.

XX PR 30-JAN-1989; 89JP-00020182.

XX PA (TANP-) TANPAKU KOGAKU KENK.

XX DR WPI; 1990-285858/38.

XX DR N-PSDB; AAQ05968.

XX PT Synthetic gene - used for coding the amino acid sequence in the hormone-
 PT combining region of human growth hormone receptor.

XX PS Disclosure; Fig 2; 11pp; Japanese.

XX CC The sequence is the same as that of the natural receptor but is encoded
 CC by a synthetic gene that has a slightly altered nucleotide sequence
 CC incorporating at least 2 new restriction sites and removing a direct
 CC repeat and a palindromic sequence

XX

SQ Sequence 249 AA;
 Query Match 88.4%; Score 38; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
 |||||
 Db 241 CEEDFY 246

RESULT 7
 AAR05045
 ID AAR05045 standard; protein; 269 AA.
 XX
 AC AAR05045;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-1990 (first entry)
 XX
 DE Soluble human growth hormone receptor.
 XX
 KW Plasmid pJ1446; human growth hormone; somatogenic receptor; mutagenesis;
 KW substitutions; active domain; hormone variants.
 XX
 OS Synthetic.
 XX
 XX WO9004788-A.
 XX
 PD 03-MAY-1990.
 XX
 PF 28-OCT-1988; 88US-00264611.
 XX
 PR 28-OCT-1988; 88US-00264611.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wells JA, Cunningham BC;
 XX
 DR WPI; 1990-164120/21.
 DR N-PSDB; AAQ04672.
 XX
 PT Identifying active domains and aminoacid(s) in polypeptide(s) - by
 PT specific substitutions, then testing modified products for interaction
 PT with target, and new polypeptide, esp. hormone etc.
 XX
 PS Disclosure; Page ?; 193pp; English.
 XX
 CC The soluble human growth hormone receptor shGhr was subcloned into pBO475
 CC to form pJ1446. E.coli W3110, degp was transformed with pJ1446 and grown
 CC in low-phosphate media in a fermentor at 30 degrees C. This 246 amino
 CC acid hGhr is produced. See also AAQ04671 and AAQ04672. (Updated on 25-MAR
 CC -2003 to correct PR field.)
 XX
 SQ Sequence 269 AA;
 Query Match 88.4%; Score 38; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
 |||||
 Db 264 CEEDFY 269

RESULT 8
 AAW10426
 ID AAW10426 standard; protein; 269 AA.
 XX
 AC AAW10426;
 XX
 DT 25-MAR-2003 (revised)
 DT 11-AUG-1997 (first entry)

XX DE Human somatogenic receptor extracellular domain.
 XX
 KW Active site; active domain; growth hormone; somatogenic receptor;
 KW mutagenesis.
 XX
 XX Homo sapiens.
 OS
 XX
 Key Location/Qualifiers
 FH 1..23
 FT /label= Sig_peptide
 FT 24..269
 FT /label= Mat_protein
 FT /note= "shGhr(aal-246)"
 XX
 XX US5580723-A.
 DN
 XX
 XX 03-DEC-1996.
 XX
 XX 02-FEB-1994; 94US-00190723.
 PF
 XX
 XX 28-OCT-1988; 88US-00264611.
 PR
 XX 26-OCT-1989; 89US-00428066.
 PR
 XX 27-APR-1992; 92US-00875204.
 PR
 XX 13-OCT-1992; 92US-00960227.
 PR
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Cunningham BC, Wells JA;
 PI
 XX
 DR WPI; 1997-033563/03.
 DR N-PSDB; AAT10426.
 XX
 PT Identification of unknown active domains in polypeptide(s) - useful for
 PT analysis of structure and function of hormones, etc.
 XX
 XX
 XX Example 3; Fig 12A-C; 86pp; English.
 XX
 CC A polypeptide (AAW10426) comprises the soluble extracellular domain of
 CC human liver growth hormone receptor (somatogenic receptor, shGhr). It was
 CC expressed in Escherichia coli transformants using a vector derived from
 CC pJ1446 (AAT47449). shGhr can be used in a novel method designed for the
 CC identification of polypeptide active domains. For human growth hormone
 CC (hGH) (see also AAW10425), this involves substituting selected amino acid
 CC segments of hGH with analogous segments from analogue polypeptides (human
 CC placenta lactogen, human prolactin and pig growth hormone) and examining
 CC the effect of the substn. on binding affinity to shGhr. Once active site
 CC regions are detd., active site amino residues (see also AAW10427-62) can
 CC be similarly identified. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 269 AA;
 Query Match 88.4%; Score 38; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
 |||||
 Db 264 CEEDFY 269

RESULT 9
 AAY31767
 ID AAY31767 standard; protein; 269 AA.
 XX
 AC AAY31767;
 XX
 DT 06-DEC-1999 (first entry)
 DT
 XX
 DE Human soluble growth hormone receptor.
 XX
 KW Growth hormone receptor; somatogenic receptor; human; pJ1446; variant;
 KW protein engineering.

```

XX OS Homo sapiens.
XX FH Key
XX FT Peptide 1..23 Location/Qualifiers
XX FT Protein /note= "signal peptide"
XX FT Protein 24..269
XX FT Protein /note= "mature protein"
XX PN US5955346-A.
XX XX
XX PD 21-SEP-1999.
XX XX
XX XX 07-JUN-1995; 95US-00476999.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 02-FEB-1994; 94US-00190723.
XX PA (GETH ) GENENTECH INC.
XX PI Cunningham BC, Wells JA;
XX DR WPI; 1999-560495/47.
XX DR N-PSDB; AAX87977.
XX PT Isolated nucleic acids encoding variants of human prolactin and placental
XX PT lactogen useful for identifying active domains within those proteins.
XX PS Example 2; Fig 12A-C; 86pp; English.
XX CC This sequence represents a human soluble growth hormone receptor (shGHR)
XX CC encoded by plasmid pJ1446 (see AAX87977). shGHR was expressed in E. coli
XX CC and was used in binding assays of human growth hormone variants. The
XX CC invention provides a method for the systematic analysis of the structure
XX CC and function of polypeptides by identifying active domains which
XX CC influence the activity of the polypeptide with a target substance, and a
XX CC method for identifying the active amino acid residues within the active
XX CC domain of a polypeptide. It also provides polypeptide variants comprising
XX CC segment-substituted and residue-substituted growth hormones, prolactins
XX CC (see AAX31764) and placental lactogens (see AAX31765). Identifying
XX CC receptor binding sites in hormones permits the rational design of
XX CC receptor specific variants
XX CC Sequence 269 AA;
XX SQ
XX Query Match 88.4%; Score 38; DB 2; Length 269;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 CEDDFY 6
XX Db 264 CEDDFY 269
XX RESULT 10
XX AAW82802
XX ID AAW82802 standard; protein; 269 AA.
XX AC AAW82802;
XX XX
XX DT 01-MAR-1999 (first entry)
XX DE Human soluble somatogenic receptor.
XX XX
XX KW Somatogenic receptor; growth hormone; human; plasmid pJ1446;
XX KW active domain.
XX OS Homo sapiens.
XX FH Key
XX FH Location/Qualifiers

```

```

FT Peptide 1..23
FT Protein /label= Sig_peptide
FT Protein 24..269
FT Protein /label= Mat_protein
XX US5834250-A.
XX PD 10-NOV-1998.
XX XX
XX PF 30-JUN-1997; 97US-00903398.
XX XX
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 06-JUN-1995; 95US-00483039.
XX PA (GETH ) GENENTECH INC.
XX PI Cunningham BC, Wells JA;
XX DR WPI; 1999-008714/01.
XX DR N-PSDB; AAV62766.
XX PT Identifying amino acids in polypeptide(s) that are involved in
XX PT interaction with target - by introducing scanning amino acid
XX PT substitutions at selected positions and screening for any change in
XX PT interaction, particularly to engineer hormones with altered properties.
XX PS Example 3; Fig 12A-J; 84pp; English.
XX CC This is the amino acid sequence of human liver soluble somatogenic
XX CC receptor, as encoded by a DNA insert of plasmid pJ1446 (see AAV62766).
XX CC The invention provides methods for the systematic analysis of the
XX CC structure and function of polypeptides by identifying active domains
XX CC which influence the activity of the polypeptide with a target substance
XX CC (for human growth hormone (see AAW82801, the target used was somatogenic
XX CC receptor). Active domains are determined by substituting selected amino
XX CC acid segments of the polypeptide with an analogous polypeptide segment,
XX CC and comparing the activity of the substituted polypeptide with that of
XX CC the native polypeptide for the target. The invention also provides
XX CC methods for identifying the active amino acids within the active domain.
XX CC The method is particularly applied to hormones. Polypeptides can be
XX CC produced that have better biological, biochemical and immunogenic
XX CC properties than wild-type proteins, e.g. human growth hormone with
XX CC increased potency but reduced diabetogenic activity and human prolactin
XX CC or placental lactogen may have increased activity at somatogenic
XX CC receptors
XX SQ Sequence 269 AA;
XX Query Match 88.4%; Score 38; DB 2; Length 269;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 CEDDFY 6
XX Db 264 CEDDFY 269
XX RESULT 11
XX AAY78429
XX ID AAY78429 standard; protein; 269 AA.
XX AC AAY78429;
XX XX
XX DT 09-MAY-2000 (first entry)
XX DE Soluble part of the somatogenic receptor encoded by plasmid pJ1446.
XX KW Human growth hormone; hGH; prolactin; placental lactogen; modification;
XX KW mutagenesis.

```

```

XX OS Homo sapiens.
XX OS Synthetic.
XX PN US6013478-A.
XX PD 11-JAN-2000.
XX PF 24-JUN-1998; 98US-00104036.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 06-JUN-1995; 95US-00483039.
XX PR 30-JUN-1997; 97US-00903398.
XX PA (GETH ) GENENTECH INC.
XX PI Wells JA, Cunningham BC;
XX PS WPI; 2000-159873/14.
XX DR N-PSDB; AAZ88448.
XX PT Recombinant production of variant polypeptides, e.g. growth hormone
XX PT variants with altered receptor specificity, using cells transfected with
XX PT DNA selected by scanning mutagenesis in at least one peptide domain.
XX PS Example 3; Fig 12; 83pp; English.
XX CC The present invention describes the production of a polypeptide variant
XX CC (I) comprising segment substituted and residue substituted growth
XX CC hormone, prolactin or placental lactogens. The method is particularly
XX CC used to produce variants of growth hormone (GH), prolactin or placental
XX CC lactogen, but may also be applied to receptors, interferons, and colony-
XX CC stimulating factors. A particular application is the production of human
XX CC GH variants with altered (decreased or increased) binding interaction
XX CC with the somatogenic receptor, i.e. compounds useful as human GH
XX CC (antagonists and which may have higher potency for stimulating other
XX CC human GH receptors, and as standards or tracers in immunoassays for human
XX CC GH. This method of DNA selection identifies the biologically active
XX CC residues in active domains, including those critical for interaction with
XX CC different targets. The present sequence represents the soluble region of
XX CC the somatogenic receptor from liver encoded by a plasmid, which is used
XX CC in the exemplification of the present invention
XX SQ Sequence 269 AA;
Query Match 88.4%; Score 38; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CEEDFY 6
Db 264 CEEDFY 269
RESULT 12
ADE82252
ID ADE82252 standard; protein; 269 AA.
XX AC ADE82252;
XX XX 29-JAN-2004 (first entry)
XX XX Plasmid pBJ1466 containing growth hormone (hGH) protein.
XX DE human growth hormone; hGH; variant; somatogenic receptor; circular.
XX KW Synthetic.
XX OS US6451561-B1.
XX PN

```

```

XX PD 17-SEP-2002.
XX PF 07-JUN-1995; 95US-00486474.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PA (GETH ) GENENTECH INC.
XX PI Wells JA, Cunningham BC;
XX PS WPI; 2003-101735/09.
XX DR N-PSDB; ADE82251.
XX PT Forming human growth hormone (hGH) variants by substitution mutation so
XX PT that the variant binds to a target for hGH, e.g. hGH receptors or human
XX PT prolactin receptors with affinity different from that of wild-type hGH.
XX PS Example 3; Fig 12A-C; 87pp; English.
XX CC This invention describes a method for generating a novel human growth
XX CC hormone (hGH) variant that binds to a target for hGH with an affinity
XX CC different from affinity of wild type hGH for the target. Human growth
XX CC hormone (hGH) has a positive binding activity with the target receptor,
XX CC the somatogenic receptor. The human prolactin (hPRL), human placental
XX CC lactogen (hPL) and porcine growth hormone (pGH) analogues, however, have
XX CC a greatly reduced activity with that target. Six segment-substituted
XX CC growth hormones were formed by substituting selected amino acid segments
XX CC of hGH with an analogous amino acid segment from the analogue. Each of
XX CC these selected segments are different and were chosen to probe either the
XX CC entire amino acid sequence of the hGH molecule or those regions which are
XX CC expected to contain the active domains. This sequence represents the
XX CC plasmid pJ1466 which contains the synthetic hGH described in the
XX CC disclosure of the invention.
XX SQ Sequence 269 AA;
Query Match 88.4%; Score 38; DB 7; Length 269;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CEEDFY 6
Db 264 CEEDFY 269
RESULT 13
AAU75499
ID AAU75499 standard; protein; 315 AA.
XX AC AAU75499;
XX XX 08-MAY-2002 (first entry)
XX DE Human fusion protein Chi 1A2.
XX KW Human; GHS1-23; human growth hormone; GH; GHR; growth hormone; receptor;
XX KW GHtopGHR SD100; GHlinkGHR; GHlinkGHRflec; pTcrnssac1; TrcHindrev;
XX KW Chi 1A2 chimera; acromegaly; gigantism; growth hormone deficiency;
XX KW Turner's syndrome; renal failure; osteoporosis; diabetes mellitus;
XX KW cancer; obesity; insulin resistance; hyperlipidaemia; hypertension;
XX KW anaemia; autoimmune disease; infectious disease; inflammatory disorder;
XX KW rheumatoid arthritis; interleukin-6 chimera; IL-6.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
XX FT Misc-difference 14
XX FT /note= "Encoded by ATG"

```


Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
Db 331 CEEDFY 336

RESULT 15

AAP92108
ID AAP92108 standard; protein; 637 AA.

XX AC

XX AAP92108;

XX DT 14-FEB-1990 (first entry)

XX DE

XX Human growth hormone receptor.

XX KW

XX Growth hormone receptor.

XX OS

XX Homo sapiens.

XX FN

XX US4857637-A.

XX PD

XX 15-AUG-1989.

XX PF

XX 12-JUN-1987; 87US-00061942.

XX PR

XX 22-MAY-1985; 85US-00737302.

XX PR

XX 07-MAY-1986; 86US-00861236.

XX PA

XX (GETH) GENENTECH INC.

XX PI

XX Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;

XX DR

XX WPI; 1989-300419/41.

XX DR

XX N-PSDE; AAN91325.

XX PT

XX Modulating growth hormone receptor activity - by immunising animal

XX PT

XX against growth hormone receptor extracellular domain deriv. to raise

XX PT

XX antiser.

XX PS

XX Disclosure; Fig 2a-c; 18pp; English.

XX CC

XX An animal can be immunised against its growth hormone receptor by

XX CC

XX vaccinating against a growth hormone receptor extracellular domain deriv.

XX CC

XX predetermined to raise polyclonal antiser.

XX CC

XX growth hormone agonist. This method enables continuous growth of target

XX CC

XX tissues without frequent hormone admin

XX SQ

Sequence 637 AA;

Query Match 88.4%; Score 38; DB 1; Length 637;

Best Local Similarity 100.0%; Pred. No. 66;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6

Db 259 CEEDFY 264

Search completed: June 9, 2004, 15:48:28

Job time : 36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 7.75676 Seconds
(without alignments)
86.807 Million cell updates/sec

Title: US-09-660-302D-7

Perfect score: 43

Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	88.4	638	2	3A3991
2	36	83.7	364	1	TVHOML
3	36	83.7	368	1	TVHOML
4	36	83.7	378	2	JC5658
5	36	83.7	400	2	JC5657
6	36	83.7	426	1	A47179
7	36	83.7	726	2	B86202
8	35	81.4	202	2	B81371
9	35	81.4	552	2	AC0609
10	35	81.4	1376	2	S63986
11	35	81.4	1822	2	S63985
12	35	81.4	3198	2	A43426
13	34	79.1	277	2	B84478
14	34	79.1	331	2	E97111
15	34	79.1	563	2	AG2393
16	34	79.1	599	2	A57701
17	34	79.1	612	2	A34967
18	34	79.1	625	2	T40742
19	34	79.1	707	1	A64047
20	33	76.7	86	2	H69321
21	33	76.7	272	2	D90597
22	33	76.7	441	2	T28411
23	33	76.7	496	2	T20926
24	32	74.4	154	2	B84973
25	32	74.4	200	2	T42678
26	32	74.4	309	2	T38671
27	32	74.4	352	2	C85909
28	32	74.4	352	2	G91064
29	32	74.4	395	1	I50376

30	32	74.4	407	2	C86202
31	32	74.4	415	2	G83863
32	32	74.4	486	2	JC1415
33	32	74.4	487	2	JC2495
34	32	74.4	488	2	I56507
35	32	74.4	491	2	A41632
36	32	74.4	531	2	G84710
37	32	74.4	581	2	B54665
38	32	74.4	606	2	A54665
39	32	74.4	647	2	S26386
40	32	74.4	676	2	A81349
41	32	74.4	740	2	F71369
42	32	74.4	796	2	T39962
43	32	74.4	893	2	S51603
44	32	74.4	898	2	S47489
45	32	74.4	976	2	A36355

ALIGNMENTS

RESULT 1

A33991

somatotropin receptor precursor - human

N;Alternate names: growth hormone receptor

N;Contains: somatotropin-binding protein, serum

C;Species: Homo sapiens (man)

C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 02-Aug-2002

C;Accession: A33991; S04530

R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R; Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989

A;Title: Characterization of the human growth hormone receptor gene and demonstration of

A;Reference number: A33991; MUID:90046742; PMID:2813379

A;Accession: A33991

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-638 <GOD>

A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; G; R; Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.; Nature 330, 537-543, 1997

A;Title: Growth hormone receptor and serum binding protein: purification, cloning and es

A;Reference number: S04530; MUID:88065896; PMID:2825030

A;Accession: S04530

A;Molecule type: mRNA

A;Residues: 1-543, 'I', 545-638 <LEU>

A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738

C;Genetics:

A;Gene: GDB:GHR

A;Cross-references: GDB:119984; OMIM:600946

A;Map position: 5p13-5p12

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status predicted <MAT>

F;265-288/Domain: transmembrane #status predicted <TM>

Query Match 88.4%; Score 38; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6

DB 259 CEEDFY 264

RESULT 2

TVHOML

transforming protein L-myc-1 - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1999

C;Accession: A27675; S01200; S09390

R;Kaye, F.; Battay, J.; Nau, M.; Brooks, B.; Seifter, E.; De Greve, J.; Birrer, M.; Saus

Mol. Cell. Biol. 8, 186-195, 1988

A;Title: Structure and expression of the human L-myc gene reveal a complex pattern of al
A;Reference number: A27675; MUID:98094386; PMID:2827002
A;Accession: A27675
A;Molecule type: DNA
A;Residues: 1-364 <KAY>
A;Cross-references: GB:M19720; NID:gl88906; PIDN:AAA59879.1; PID:g386964
R;DePinho, R.A.; Hatton, K.S.; Tesfaye, A.; Yancopoulos, G.D.; Alt, F.W.
Genes Dev. 1, 1311-1326, 1987
A;Title: The human myc gene family: structure and activity of L-myc and an L-myc pseudog
A;Reference number: S01200; MUID:88112807; PMID:332939
A;Accession: S01200
A;Molecule type: DNA
A;Residues: 1-364 <DBP>
R;Ikigaki, N.; Minna, J.; Kennett, R.H.
EMBO J. 8, 1793-1799, 1989
A;Title: The human L-myc gene is expressed as two forms of protein in small cell lung ca
A;Reference number: S09390; MUID:8935654; PMID:2548855
A;Accession: S09390
A;Status: preliminary
A;Molecule type: protein
A;Residues: 165-179 <IKE>
C;Genetics:
A;Gene: GDB:MYCL1
A;Cross-references: GDB:120706; OMIM:164850
A;Map position: 1p32-1p32
A;Introns: 166/1
C;Superfamily: myc transforming protein; myc transforming protein homology
C;Keywords: DNA binding; nucleus; transforming protein
F;1-364/Domain: myc transforming protein homology <MYC>

Query Match 83.7%; Score 36; DB 1; Length 364;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEEDFYR 7
Db 15 CGEDFYR 21

RESULT 3
TVMSML
transforming protein L-myc - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
C;Accession: S03017
R;Legouy, E.; DePinho, R.; Zimmerman, K.; Collum, R.; Yancopoulos, G.; Mitsock, L.; Kri
EMBO J. 6, 3359-3366, 1987
A;Title: Structure and expression of the murine L-myc gene.
A;Reference number: S03017; MUID:88111523; PMID:2828024
A;Accession: S03017
A;Molecule type: DNA
A;Residues: 1-368 <LRG>
A;Cross-references: GB:X13945; GB:X06183; GB:X13949; GB:Y00082; NID:g53287; PIDN:CAA3212
C;Genetics:
A;Gene: L-myc
C;Superfamily: myc transforming protein; myc transforming protein homology
C;Keywords: DNA binding; leucine zipper; nucleus; transforming protein
F;1-368/Domain: myc transforming protein homology <MYC>
F;337-365/Region: leucine zipper motif

Query Match 83.7%; Score 36; DB 1; Length 368;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEEDFYR 7
Db 15 CGEDFYR 21

RESULT 4
JC5658
LIM domain-containing homeodomain LH-2B - chicken
C;Species: Gallus gallus (chicken)

C;Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 15-Oct-1999
C;Accession: JC5658
R;Nohno, T.; Kawakami, Y.; Wada, N.; Ishikawa, T.; Ohuchi, H.; Noji, S.
Biochem. Biophys. Res. Commun. 238, 506-511, 1997
A;Title: Differential expression of the two closely related LIM-class homeobox genes LH
A;Reference number: JC5657; MUID:97446014; PMID:9299541
A;Accession: JC5658
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-378 <NOH>
A;Cross-references: GB:L35566; NID:g556037; PIDN:AAA50258.1; PID:g556038
C;Comment: This protein plays a role in the determination and specification of the proxi
C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homol
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;50-100/Domain: LIM domain 1 #status predicted <LD1>
F;52-104/Domain: LIM metal-binding repeat homology <LIM>
F;103-169/Domain: LIM domain 2 #status predicted <LD2>
F;114-167/Domain: LIM metal-binding repeat homology <LIM1>
F;246-310/Domain: homeodomain #status predicted <HOM>
F;249-305/Domain: homeobox homology <HOX>

Query Match 83.7%; Score 36; DB 2; Length 378;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFYR 7
Db 101 CKEDYR 107

RESULT 5
JC5657
LIM domain-containing homeodomain LH-2A - chicken
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-1997 #sequence_revision 17-Nov-1997 #text_change 20-Jun-2000
C;Accession: JC5657
R;Nohno, T.; Kawakami, Y.; Wada, N.; Ishikawa, T.; Ohuchi, H.; Noji, S.
Biochem. Biophys. Res. Commun. 238, 506-511, 1997
A;Title: Differential expression of the two closely related LIM-class homeobox genes LH
A;Reference number: JC5657; MUID:97446014; PMID:9299541
A;Accession: JC5657
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-400 <NOH>
A;Cross-references: GB:AB005882; NID:g2340818; PIDN:BAA21846.1; PID:g2340819
C;Comment: This protein plays a role in the determination and specification of the proxi
C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homol
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;52-102/Domain: LIM domain 1 #status predicted <LD1>
F;54-106/Domain: LIM metal-binding repeat homology <LIM1>
F;105-171/Domain: LIM domain 2 #status predicted <LD2>
F;116-169/Domain: LIM metal-binding repeat homology <LIM>
F;258-322/Domain: homeodomain #status predicted <HOM>
F;261-317/Domain: homeobox homology <HOX>

Query Match 83.7%; Score 36; DB 2; Length 400;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFYR 7
Db 103 CKEDYR 109

RESULT 6
A47179
homeotic protein LH-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Jul-1997
C;Accession: A47179
R;Xu, Y.; Baldassare, M.; Fisher, P.; Rathbun, G.; Oltz, E.M.; Yancopoulos, G.D.; Jesse
Proc. Natl. Acad. Sci. U.S.A. 90, 227-231, 1993
A;Title: LH-2: a LIM/homeodomain gene expressed in developing lymphocytes and neural cel

A;Reference number: A47179; MUID:93126348; PMID:7678338
 A;Accession: A47179
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-426 <XU1>

A;Cross-references: GB:I06804
 A;Experimental source: brain
 A;Note: sequence inconsistent with the nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIN:122101, NCBI:122102)
 C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homology
 C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc
 F;52-104/Domain: LIM metal-binding repeat homology <LIM1>
 F;114-167/Domain: LIM metal-binding repeat homology <LIM2>
 F;265-321/Domain: homeobox homology <HOX>

Query Match 83.7%; Score 36; DB 1; Length 426;
 Best Local Similarity 71.4%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 |:|:|:
 Db 101 CKEDYR 107

RESULT 7

B86202
 hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: B86202
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federespiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: B86141; MUID:21016719; PMID:11130712
 A;Accession: B86202
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-726 <STO>
 A;Cross-references: GB:AE005172; NID:g7523705; PIDN:AAF63144.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 83.7%; Score 36; DB 2; Length 726;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 |:|:|:
 Db 633 CEEDYR 639

RESULT 8

B81371
 hypothetical protein Cj0963 [imported] - Campylobacter jejuni (strain NCTC 11168)
 C;Species: Campylobacter jejuni
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C;Accession: B81371
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hvt
 A;Reference number: B81250; MUID:20150912; PMID:10688204
 A;Accession: B81371
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-202 <PAR>

A;Cross-references: GB:AL139076; GB:AL111168; NID:g9698128; PIDN:CAB73220.1; PID:g96984
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj0963

Query Match 81.4%; Score 35; DB 2; Length 202;
 Best Local Similarity 83.3%; Pred. No. 17;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
 |:|:|:
 Db 99 CEEDFY 104

RESULT 9

AC0609
 conserved hypothetical protein STY0935 [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AC0609
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AC0609
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-552 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD05341.1; PID:g16502105; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY0935

Query Match 81.4%; Score 35; DB 2; Length 552;
 Best Local Similarity 71.4%; Pred. No. 45;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 |:|:|:
 Db 103 CEEDFYR 109

RESULT 10

S63986
 collagen alpha 5 chain - sea urchin (Strongylocentrotus purpuratus) (fragment)
 C;Species: Strongylocentrotus purpuratus (purple urchin)
 C;Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 25-Apr-1997
 C;Accession: S63986; S64638
 R;Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.
 Eur. J. Biochem. 234, 59-65, 1995
 A;Title: Characterization of two genes coding for a similar four-cysteine motif of the a
 A;Reference number: S63985; MUID:96096722; PMID:8529669
 A;Accession: S63986
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-1376 <EXP>

A;Cross-references: EMBL:X89804
 R;Exposito, J.Y.
 submitted to the EMBL Data Library, July 1995
 A;Reference number: S64637
 A;Accession: S64638
 A;Molecule type: DNA
 A;Residues: 1-658,'G',660-870,'G',872-901,'H',903-1185,'T',1187-1214,'Y',1216-1376 <EXW>
 A;Cross-references: EMBL:X89804
 C;Genetics:

A;Gene: COLP5alpha
 A;Introns: 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1; 1093/1; 1236/1
 C;Superfamily: von Willebrand factor type C repeat homology
 C;Keywords: extracellular matrix
 F;15-73/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 81.4%; Score 35; DB 2; Length 1376;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
|||||
Db 1335 CEEDYY 1340

RESULT 11

A43426
collagen alpha 2 chain precursor - sea urchin (Strongylocentrotus purpuratus) (fragment)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 20-Jul-1996 #sequence_revision 01-Nov-1996 #text_change 15-Sep-2003
C:Accession: S63985; S64637
R:Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.
Eur. J. Biochem. 234, 59-65, 1995
A:Title: Characterization of two genes coding for a similar four-cysteine motif of the a
A:Reference number: S63985; MUID:96096722; PMID:8529669
A:Accession: S63985
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1822 <EXP>
A:Cross-references: EMBL:X89806
R:Exposito, J.Y.
submitted to the EMBL Data Library, July 1995
A:Reference number: S64637
A:Accession: S64637
A:Molecule type: DNA
A:Residues: 1-381, 'DT', 384-677, 'N', 679-1010, 'L', 1012-1822 <EXW>
A:Cross-references: EMBL:X89806
C:Genetics:
A:Gene: COL2A1alpha

A:Introns: 33/1; 106/1; 169/2; 254/1; 395/1; 460/3; 534/1; 678/1; 743/3 817/1; 965/1; 11
F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>
Query Match 81.4%; Score 35; DB 2; Length 1822;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
|||||
Db 1781 CEEDYY 1786

RESULT 12

A43426
collagen alpha 2 fibrillar chain precursor - sea urchin (Strongylocentrotus purpuratus)
C:Species: Strongylocentrotus purpuratus (purple urchin)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003
C:Accession: A43426
R:Exposito, J.Y.; D'Alessio, M.; Ramirez, F.
J. Biol. Chem. 267, 17404-17408, 1992
A:Title: Novel amino-terminal propeptide configuration in a fibrillar procollagen underg
A:Reference number: A43426; MUID:92381062; PMID:1380962
A:Accession: A43426
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-3198 <EXP>
A:Cross-references: GB:M92041; NID:gl51448; PIDN:AAA30040.1; PID:gl51449
A:Note: sequence extracted from NCBI backbone (NCBIP:111965)
F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>
F:2978-3198/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 81.4%; Score 35; DB 2; Length 3198;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
|||||
Db 1778 CEEDYY 1783

RESULT 13

E84478
hypothetical protein At2g06570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: E84478

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84478
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-277 <STO>
A:Cross-references: GB:AF002093; NID:g4584359; PIDN:AAD25153.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g06570
A:Map position: 2

Query Match 79.1%; Score 34; DB 2; Length 277;
Best Local Similarity 83.3%; Pred. No. 36;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6
|||||
Db 204 CEEDFF 209

RESULT 14

E97111
L-asparaginase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: E97111

R:Nally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4836, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: E97111
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <KUR>

A:Cross-references: GB:AF001437; PIDN:AAK79680.1; PID:gl5024680; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC1714
C:Superfamily: asparaginase

Query Match 79.1%; Score 34; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEDFYR 7
|||||
Db 323 EEDFYR 328

RESULT 15

AG2393
DNA repair helicase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG2393

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A:Reference number: AB1807; MUID:21595285; PMID:11759640

A;Accession: AG2393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-563 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA076402.1; PID:gl7133840; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4703

Query Match 79.1%; Score 34; DB 2; Length 563;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
||| |
Db 531 CEEDFAR 537

Search completed: June 9, 2004, 15:52:18
Job time : 8.75676 secs

This Page Blank (uspto)

RP VARIANT LARON DWARFISM HIS-170.
 RX MEDLINE=94185645; PubMed=8137822;
 RA Duesquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R.,
 RA Savage M.O., Preece M.A., Craescu C.T., Plouquit Y., Goossens M.,
 RA Anselm S.;
 RT "A single amino acid substitution in the exoplasmic domain of the
 RT human growth hormone (GH) receptor confers familial GH resistance
 RT (Laron syndrome) with positive GH-binding activity by abolishing
 RT receptor homodimerization.";
 RL EMBO J. 13:1386-1395(1994).
 [7]
 RN VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242.
 RP MEDLINE=96013502; PubMed=7565946;
 RX Goddard A.D., Covello R., Luoh S.-M., Clarkson T., Attie K.M.,
 RA Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.W.S.;
 RT "Mutations of the growth hormone receptor in children with idiopathic
 RT short stature.";
 RL New Engl. J. Med. 333:1093-1098(1995).
 [8]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.
 RP MEDLINE=92196577; PubMed=1549776;
 RX de Vos A.M., Uitsch M., Kossiakoff A.A.;
 RA "Human growth hormone and extracellular domain of its receptor:
 RT crystal structure of the complex.";
 RL Science 255:306-312(1992).
 [9]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.
 RP MEDLINE=97113023; PubMed=8943276;
 RX Sundstroem M., Lundqvist T., Roedien J., Giebel L.B., Milligan D.,
 RA Norstedt G.;
 RT "Crystal structure of an antagonist mutant of human growth hormone,
 RT G120R, in complex with its receptor at 2.9-A resolution.";
 RL J. Biol. Chem. 271:32197-32203(1996).
 [10]
 RN VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579.
 RP MEDLINE=93318093; PubMed=10391209;
 RX Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Iane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 [11]
 RN ERRATUM.
 RP Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Iane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DISEASE: Defects in GHR are a cause of Laron dwarfism
 CC [MIM:262500]; also known as pituitary dwarfism II (Laron-type
 CC pituitary dwarfism or Laron syndrome (LS)).
 CC -!- DISEASE: Defects in GHR are a cause of idiopathic short stature
 CC [MIM:600946].
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
 CC Subfamily 1.
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 DR EMBL; X06562; CAA29808.1; -;
 DR EMBL; M28466; AAA52555.1; -;
 DR EMBL; M28458; AAA52555.1; JOINED.

DR EMBL; M28459; AAA52555.1; JOINED.
 DR EMBL; M28460; AAA52555.1; JOINED.
 DR EMBL; M28461; AAA52555.1; JOINED.
 DR EMBL; M28462; AAA52555.1; JOINED.
 DR EMBL; M28463; AAA52555.1; JOINED.
 DR EMBL; M28464; AAA52555.1; JOINED.
 DR EMBL; M28465; AAA52555.1; JOINED.
 DR PIR; A33991; A33991.
 DR PDB; 3HR; 30-APR-94.
 DR PDB; 1HW; 19-NOV-97.
 DR PDB; 1HW; 19-NOV-97.
 DR PDB; 1AXI; 28-JAN-98.
 DR PDB; 1A22; 29-APR-98.
 DR PDB; 1KF9; 20-NOV-02.
 DR Genew; HGNC:4263; GHR.
 DR MIM; 600946; -;
 DR MIM; 262500; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004903; F:growth hormone receptor activity; TAS.
 DR GO; GO:0007150; P:growth pattern; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003528; Hemtopoptn_L_Fl.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO REC L Fl; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;
 KW Dwarfism; Polymorphism; Disease mutation.
 FT SIGNAL 1
 FT CHAIN 19 638
 FT DOMAIN 19 264
 FT TRANSMEM 265 288
 FT DOMAIN 289 638
 FT DOMAIN 145 252
 FT DISULFID 56 66
 FT DISULFID 101 112
 FT DISULFID 126 140
 FT CARBOHYD 46 46
 FT CARBOHYD 115 115
 FT CARBOHYD 156 156
 FT CARBOHYD 161 161
 FT CARBOHYD 200 200
 FT VARIANT 62 62
 FT VARIANT 89 89
 FT VARIANT 114 114
 FT VARIANT 143 143
 FT VARIANT 162 162
 FT VARIANT 170 170
 FT VARIANT 179 179
 FT VARIANT 179 179
 FT VARIANT 179 179
 FT VARIANT 229 229
 FT VARIANT 229 229
 FT VARIANT 242 242
 FT VARIANT 440 440
 FT VARIANT 495 495
 FT VARIANT 544 544
 FT
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 E -> K (in idiopathic short stature).
 /FTid=VAR_002708.
 R -> K (in Laron dwarfism).
 /FTid=VAR_002709.
 F -> S (in Laron dwarfism).
 /FTid=VAR_002710.
 V -> A (in Laron dwarfism).
 /FTid=VAR_002711.
 V -> D (in Laron dwarfism).
 /FTid=VAR_002712.
 D -> H (in Laron dwarfism; abolish
 receptor homodimerization).
 /FTid=VAR_002713.
 R -> C (in Laron dwarfism and idiopathic
 short stature).
 /FTid=VAR_002714.
 R -> H (in dbSNP:6181).
 /FTid=VAR_013937.
 R -> G (in Laron dwarfism).
 /FTid=VAR_002715.
 R -> H (in dbSNP:6177).
 /FTid=VAR_013938.
 E -> D (in idiopathic short stature).
 /FTid=VAR_002716.
 C -> F (in dbSNP:6182).
 /FTid=VAR_013939.
 P -> T (in dbSNP:6183).
 /FTid=VAR_013940.
 I -> L (in dbSNP:6180).
 /FTid=VAR_013941.

Qy 1 CEEDFY 6
|||||

```

FT NON_TER 1 1
FT NON_CONS 11 12
FT VARIANT 13 13 F -> I.
FT VARIANT 14 14 Y -> E.
FT VARIANT 15 15 R -> K.
FT NON_TER 20 20
FT SEQUENCE 20 AA; 2438 MW; 9F4E4678B086C298 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 0.51;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 9 CDKDFYR 15

RESULT 5
MYCL_HUMAN STANDARD; PRT; 364 AA.
ID MYCL_HUMAN Q9NUE9;
AC P12524;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE L-myc-1 proto-oncogene protein.
DE MYCL1 OR MYCL OR LMYC.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88094386; PubMed=2827002;
RA Kaye F., Battey J., Nau M., Brooks B., Seifter E., de Greve J.,
RA Barrer M., Sausville E., Minna J.;
RT "Structure and expression of the human L-myc gene reveal a complex
RT pattern of alternative mRNA processing.";
RL Mol. Cell. Biol. 8:186-195(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88112807; PubMed=3322939;
RA Depinho R.A., Hatton K.S., Tesfaye A., Yancopoulos G.D., Alt F.W.;
RT "The human myc gene family: structure and activity of L-myc and an
RT L-myc pseudogene.";
RL Genes Dev. 1:1311-1326(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Ellington A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein. Binds DNA as an heterodimer with MAX.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; M19720; AAA59879.1; -
CC EMBL; X07262; CAA30248.1; -
CC EMBL; X07263; CAA30249.1; -
CC EMBL; AL033527; CAB75682.1; -
CC PIR; A27675; TVHML.
CC HSP; P25912; 1HLO.
CC TRANSFAC; T02385; -
CC Genew; HGNC:7555; MYCL1.
CC MIM; 164850; -
CC GO; GO:0003677; F:DNA binding; NAS.
CC InterPro; IPR001092; HLH_basic.

```

```

DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF0010; HLH; 1.
DR Pfam; PF01056; MYC_N term; 1.
DR PRINTS; PR00044; LEUZIPPRMYC.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH; 1.
KW Nuclear protein; DNA-binding; Proto-oncogene.
FT DNA BIND 282 294 BASIC DOMAIN.
FT DOMAIN 295 334 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 333 361 LEUCINE-ZIPPER (POTENTIAL).
FT CONFLICT 362 362 S -> T (IN REF. 3).
SQ SEQUENCE 364 AA; 40312 MW; 58F8A71A1C2ED6D4 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 364;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 15 CGEDFYR 21

RESULT 6
MYCL_MOUSE STANDARD; PRT; 368 AA.
ID MYCL_MOUSE P10166;
AC P10166;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE L-myc proto-oncogene protein.
DE MYCL1 OR MYCL OR LMYC1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=88111523; PubMed=2828024;
RA Legouy E., Depinho R.A., Zimmerman K., Collum R., Yancopoulos G.D.,
RA Mitsock L., Kriz R., Alt F.W.;
RT "Structure and expression of the murine L-myc gene.";
RL EMBO J. 6:3359-3366(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Marra M.A.;
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein. Binds DNA as an heterodimer with MAX.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; X13945; CAA32128.1; --
 DR EMBL; BC053059; AAH53059.1; --
 DR PIR; S03017; TVMSM.
 DR HSP; P25912; IHLO.
 DR TRANSFAC; T02387; --
 DR MGD; MGI:96799; Lmycl.
 DR InterPro; IPR001092; HLH basic.
 DR InterPro; IPR002418; TF_Myc.
 DR Pfam; PF00010; HLH; 1_Myc.
 DR Pfam; PF01056; Myc_N_term; 1.
 DR PRINTS; PR00044; LEUZIPPRMYC.
 DR SMART; SM00353; HLH; 1.
 DR PROSITE; PS00888; HLH; 1.
 DR Nuclear protein; DNA-binding; Proto-oncogene.
 FT DNA_BIND 286 298 BASIC DOMAIN
 FT DOMAIN 299 338 HELIX-LOOP-HELIX MOTIF.
 FT DOMAIN 337 365 LEUCINE-ZIPPER (POTENTIAL).
 SQ SEQUENCE 368 AA; 40848 MW; 9174F6FD7C03321E CRC64;

Query Match 83.7%; Score 36; DB 1; Length 368;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 | | | | |
 DB 15 CGEDFYR 21

RESULT 7
 LHX9_HUMAN
 ID LHX9_HUMAN STANDARD; PRT; 388 AA.
 AC Q9N069; Q9BYU6; Q9NQ70;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE LIM/homeobox protein Lhx9.
 GN LHX9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=21291005; PubMed=11397841;
 RA Ottolenghi C., Moreira-Filho C., Mendonca B.B., Barbieri M.,
 RA Fellous M., Berkovitz G.D., McElreavey K.;
 RT "Absence of mutations involving the LIM homeobox domain gene LHX9 in
 RT 46,Xy gonadal agenesis and dysgenesis.";
 RL J. Clin. Endocrinol. Metab. 86:2465-2469(2001).
 CC -!- FUNCTION: Involved in gonadal development (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: Contains 1 homeobox domain.
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; AJ277915; CAB97493.1; --
 DR EMBL; AJ277916; CAB98128.1; ALT SEQ.
 DR EMBL; AJ277917; CAB98128.1; JOINED.

DR EMBL; AJ277918; CAB98128.1; JOINED.
 DR EMBL; AJ277919; CAB98128.1; JOINED.
 DR EMBL; AJ277920; CAB98128.1; JOINED.
 DR EMBL; AJ296272; CAB33174.1; --
 DR HSP; P06601; 1FJL.
 DR Genew; HGNC:14222; LHX9.
 DR MIM; 606066; --
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR InterPro; IPR007107; LIM_homeo.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOK; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
 KW Metal-binding; Zinc.
 FT DOMAIN 62 114 LIM 1.
 FT DOMAIN 124 177 LIM 2.
 FT DNA_BIND 258 317 HOMEBOX.
 SQ SEQUENCE 388 AA; 42903 MW; A4DC8B914D7C3B66 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 388;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 | | | | |
 DB 111 CKEDFYR 117

RESULT 8
 LHX9_MOUSE
 ID LHX9_MOUSE STANDARD; PRT; 388 AA.
 AC Q9WHZ2; Q9QYQ5; Q9QYQ6; Q9Q200; Q9WU44;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE LIM/homeobox protein Lhx9.
 GN LHX9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-300 FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=99098964; PubMed=9880598;
 RA Retaux S., Rogard M., Bach I., Failli V., Beason M.J.;
 RT "Lhx9: a novel LIM-homeodomain gene expressed in the developing
 RT forebrain.";
 RL J. Neurosci. 19:783-793(1999).
 RN [2]
 RP SEQUENCE OF 11-388 FROM N.A.
 RC STRAIN=NIH Swiss;
 RX MEDLINE=99264291; PubMed=10330499;
 RA Bertuzzi S., Porter F.D., Pitts A., Kumar M., Agulnick A., Wassif C.,
 RA Westphal H.;
 RT "Characterization of Lhx9, a novel LIM/homeobox gene expressed by the
 RT pioneer neurons in the mouse cerebral cortex.";
 RL Mech. Dev. 81:193-198(1999).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=20221375; PubMed=10756098;
 RA Failli V., Rogard M., Mattei M.-G., Vernier P., Retaux S.;
 RT "Lhx9 and Lhx9alpha LIM-homeodomain factors: genomic structure,
 RT expression patterns, chromosomal localization, and phylogenetic


```
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS00023; LIM DOMAIN 2; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 53 105 LIM 1.
FT DOMAIN 115 168 LIM 2.
FT DOMAIN 187 196 POLY-ALA.
FT DOMAIN 266 325 HOMEBOX.
FT DOMAIN 307 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT CONFLICT 22 28 AKSEAPA -> QERGR (IN REF. 1).
FT CONFLICT 54 54 A -> G (IN REF. 1).
FT CONFLICT 107 107 Y -> YPSLHGPI (IN REF. 2).
FT CONFLICT 187 187 A -> Q (IN REF. 1).
FT CONFLICT 190 192 AAA -> RAR (IN REF. 1).
FT CONFLICT 196 196 MISSING (IN REF. 1).
FT CONFLICT 241 242 NA -> TR (IN REF. 1).
FT CONFLICT 391 406 GHPSPSQTLTNLF -> AMSLTAPHKRLLPFTSNDSP
SQ SEQUENCE 406 AA; 44373 MW; DF73AAC81867D30D CRC64;

Query Match 83.7%; Score 36; DB 1; Length 406;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEDDYR 7
Db 102 CKEDYR 108

RESULT 10
LHX2_MOUSE
ID LHX2_MOUSE STANDARD; PRT; 406 AA.
AC Q9Z0S2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx2.
GN LHX2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99162575; PubMed=10051612;
RA Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M.,
RA Rodriguez-Esteban C., Izpisua-Belmonte J.-C., Botas J.;
RT "Conservation of the expression and function of apterous orthologs in
RT Drosophila and mammals."
RL Proc. Natl. Acad. Sci. U.S.A. 96:2165-2170(1999).
CC -!- FUNCTION: Transcriptional regulatory protein involved in the
CC control of cell differentiation in developing lymphoid and neural
CC cell types (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; AF124734; AAD20012.1; --
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T01969; --
DR MGD; MGI:96785; Lhx2.
DR GO; GO:0007498; Pinesoderm development; IMP.
DR GO; GO:0007399; Pinesodermogenesis; IMP.
```

```
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS00023; LIM DOMAIN 2; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 53 105 LIM 1.
FT DOMAIN 115 168 LIM 2.
FT DOMAIN 187 196 POLY-ALA.
FT DNA_BIND 266 325 HOMEBOX.
FT DOMAIN 307 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 406 AA; 44419 MW; FE7B4E76454D6A90 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 406;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEDDYR 7
Db 102 CKEDYR 108

RESULT 11
LHX2_RAT
ID LHX2_RAT STANDARD; PRT; 426 AA.
AC P36198;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE LIM/homeobox protein Lhx2 (Homeobox protein Lhx-2).
GN LHX2 OR LHX2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93126348; PubMed=7678338;
RA Xu Y., Baldassare M., Fisher P., Rathbun G., Oltz E.M.,
RA Yancopoulos G.D., Jessell T.M., Alt F.W.;
RT "Lhx-2: a LIM/homeodomain gene expressed in developing lymphocytes and
RT neural cells."
RL Proc. Natl. Acad. Sci. U.S.A. 90:227-231(1993).
CC -!- FUNCTION: Transcriptional regulatory protein involved in the
CC control of cell differentiation in developing lymphoid and neural
CC cell types.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: Found in discrete regions of the developing
CC CNS, primarily in diencephalic and telencephalic structures and
CC a subset of lymphoid tissues. Also found in embryonic spinal chord
CC and fetal liver.
CC -!- DEVELOPMENTAL STAGE: Expressed in developing lymphocytes and
CC neural cells. Maximal expression is found in pre-B-lymphocytes.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

```

CC -----
DR EMBL: L06804; -; NOT_ANNOTATED_CDS.
DR HSP: P06601; 1FJL.
DR TRANSFAC; T01966; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00478; LIM_DOMAIN 1; 2.
DR PROSITE; PS00023; LIM_DOMAIN 2; 2.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 52 104 LIM 1.
FT DOMAIN 114 167 LIM 2.
FT DNA_BIND 264 323 HOMEBOX.
FT DOMAIN 305 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 426 AA; 47418 MW; DC8FA3DB4572BB40 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 426;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 101 CKEDYR 107

RESULT 12
COLB ARATH
ID COLB ARATH STANDARD; PRT; 372 AA.
AC Q9SSE5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Zinc finger protein constans-like 11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delshy M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erffle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Landie M., Berger-Ilauro C., Fumelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Cready T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.B., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

```

```

RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shingo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Belongs to the CONSTANS family.
CC -!- SIMILARITY: Contains 2 B box-type zinc fingers.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AC009176; AAP13083.1; -.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR002926; Znf_Constans.
DR Pfam; PF00643; zf-B_box; 2.
DR ProDom; PD007661; Znf_constans; 1.
DR SMART; SM00336; BBOX; 2.
DR PROSITE; PS00119; ZF_BBOX; 2.
KW Zinc-finger; Nuclear protein; Repeat; Multigene family.
FT ZN_FING 5 47 B_BOX-TYPE 1.
FT ZN_FING 48 99 B_BOX-TYPE 2 (ATYPICAL).
FT DOMAIN 77 83 POLY-ASN.
FT DOMAIN 84 90 POLY-SER.
SQ SEQUENCE 372 AA; 40754 MW; 188F18BB283D7479 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 372;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6
Db 181 CEEDFY 186

RESULT 13
CEL_MOUSE
ID CEL_MOUSE STANDARD; PRT; 599 AA.
AC Q4285;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (BAL)
DE (Bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol
DE esterase) (cholesterol esterase) (pancreatic lysophospholipase).
GN CEL OR Lip1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Mammary gland;
RX MEDLINE=96096531; PubMed=8522186;
RA Mackay K., Lawn R.M.;
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lactating mammary gland;
RX MEDLINE=96079098; PubMed=8530060;
RA Lidmer A.S., Kannus M., Lundberg L., Bjursell G., Nilsson J.;
RA "Molecular cloning and characterization of the mouse carboxyl ester
RT lipase gene and evidence for expression in the lactating mammary

```

```

RT gland.";
RL Genomics 29:115-122(1995).
CC -!- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT
CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
CC OF DIETARY TRIGLYCERIDES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U33169; AAA92088.1; -.
CC DR EMBL; U37386; AAC52279.1; -.
CC DR PIR; A57701; A57701.
CC DR HSSP; P30122; 2BCE.
CC DR SWISS-2DPAGE; Q64285; MOUSE.
CC DR MGD; MGI:88374; Cel.
CC DR GO; GO:0046514; P:ceramide catabolism; IMP.
CC DR InterPro; IPR002018; CarboxylesteraseB.
CC DR InterPro; IPR000379; Ser_estr.
CC DR Pfam; PF00135; Coesterase; 1.
CC DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;
CC Repeat; Signal.
CC FT SIGNAL 1 20
CC FT CHAIN 21 599
CC FT ACT_SITE 214 214
CC FT ACT_SITE 340 340
CC FT ACT_SITE 455 455
CC FT DISULFID 84 100
CC FT DISULFID 266 277
CC FT DOMAIN 559 588
CC FT REPEAT 559 569
CC FT REPEAT 570 580
CC FT REPEAT 581 588
CC FT CARBOHYD 207 207
CC FT CARBOHYD 325 325
CC SQ SEQUENCE 599 AA; 65813 MW; 9E4428FDFCA8602E CRC64;
CC
CC Query Match 79.1%; Score 34; DB 1; Length 599;
CC Best Local Similarity 100.0%; Pred. No. 44;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 REDFVR 7
CC DB 361 EDFVR 366
CC
CC RESULT 14
CC CEL RAT
CC ID CEL RAT STANDARD; PRT; 612 AA.
CC AC P07882; P14722;
CC DT 01-AUG-1988 (Rel. 08, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (BAL)
CC DE (Bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol
CC DE esterase) (Cholesterol esterase) (Pancreatic lysophospholipase).
CC CEL.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC OX NCBI_TaxID=10116;

```

```

[1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
RX MEDLINE=90089378; PubMed=2688744;
RA Kissel J.A., Fontaine R.N., Turck C.W., Brockman H.L., Hui D.Y.;
RT "Molecular cloning and expression of cDNA for rat pancreatic
RT cholesterol esterase.",
RL Biochim. Biophys. Acta 1006:227-237(1989).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=87242339; PubMed=3593682;
RA Han J.H., Stratawa C., Rutter W.J.;
RT "Isolation of full-length putative rat lysophospholipase cDNA using
RT improved methods for mRNA isolation and cDNA cloning.",
RL Biochemistry 26:1617-1625(1987).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=91299758; PubMed=2069957;
RA Fontaine R.N., Carter C.P., Hui D.Y.;
RT "Structure of the rat pancreatic cholesterol esterase gene.",
RL Biochemistry 30:7008-7014(1991).
[4]
ACTIVE SITE SER-214.
RX MEDLINE=91009095; PubMed=2211595;
RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
RT "Identification of the active site serine in pancreatic cholesterol
RT esterase by chemical modification and site-specific mutagenesis.",
RL J. Biol. Chem. 265:16801-16806(1990).
[5]
ACTIVE SITE HIS-455.
RX MEDLINE=91154187; PubMed=1999399;
RA Dipersio L.P., Fontaine R.N., Hui D.Y.;
RT "Site-specific mutagenesis of an essential histidine residue in
RT pancreatic cholesterol esterase.",
RL J. Biol. Chem. 266:4033-4036(1991).
CC -!- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT
CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION
CC OF DIETARY TRIGLYCERIDES.
CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -!- CATALYTIC ACTIVITY: A sterol ester + H(2)O = a sterol + a fatty
CC acid.
CC -!- ENZYME REGULATION: Activated by bile salts containing a 7-hydroxyl
CC group.
CC -!- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE PANCREAS AND THEN
CC TRANSPORTED TO THE INTESTINE.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X16054; CAA34189.1; -.
CC DR EMBL; M15893; AAA41540.1; -.
CC DR EMBL; M69157; AAB46376.1; -.
CC DR PIR; A34967; A34967.
CC DR HSSP; P30122; 2BCE.
CC DR InterPro; IPR002018; CarboxylesteraseB.
CC DR InterPro; IPR000379; Ser_estr.
CC DR Pfam; PF00135; Coesterase; 1.
CC DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
CC DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
CC KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;
CC Repeat; Signal.
CC FT SIGNAL 1 20
CC FT CHAIN 21 612
CC FT ACT_SITE 214 214
CC FT ACT_SITE 340 340
CC FT ACT_SITE 455 455

```

```

FT DISULFID      84 100      BY SIMILARITY.
FT DISULFID     266 277      BY SIMILARITY.
FT CARBOHYD     207 207      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DOMAIN       556 599      4 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED
                             REGION.
FT REPEAT       556 566      1.
FT REPEAT       567 577      2.
FT REPEAT       578 588      3.
FT REPEAT       589 599      4.
FT MUTAGEN     440 440      H->Q,R,A,S,D: ABOLISHES ACTIVITY.
FT CONFLICT     26 26       V -> L (IN REF. 2).
FT CONFLICT     154 154     G -> A (IN REF. 2).
FT CONFLICT     217 217     A -> G (IN REF. 2).
FT CONFLICT     219 219     S -> I (IN REF. 2).
FT CONFLICT     419 419     M -> T (IN REF. 3).
FT CONFLICT     513 513     T -> M (IN REF. 2 AND 3).
FT CONFLICT     576 577     GG -> VV (IN REF. 3).
FT CONFLICT     608 609     GP -> VA (IN REF. 3).
FT CONFLICT     611 611     G -> A (IN REF. 3).
SQ SEQUENCE    612 AA; 67040 MW; 1569CE4EA71ED02A CRC64;

Query Match      79.1%; Score 34; DB 1; Length 612;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EEDFYR 7
      |||||
Db     361 EEDFYR 366

RESULT 15
NRDD HAEIN
ID NRDD HAEIN STANDARD; PRT; 707 AA.
AC P43752;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2).
GN NRDD OR HI0075.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized
CC thioredoxin + H(2)O = ribonucleoside triphosphate + reduced
CC thioredoxin.
CC -!- SUBUNIT: Tetramer consisting of 2 alpha (Nrdd) and 2 beta (NrDG)
CC subunits (By similarity).
CC -!- SIMILARITY: STRONG, TO E.COLI AND T4 NRDD.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
```

```

CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U32693; AAC21751.1; -.
DR EIR; A64047; A64047.
DR HSSP; P07071; 1B8B.
DR TIGR; HI0075; -.
DR InterPro; IPR005144; ATP.
DR InterPro; IPR001150; Form_actrans_GR.
DR Pfam; PF03477; ATP-cone; 1.
DR Pfam; PF01228; Gly radical; 1.
DR PROSITE; PS00850; GLY_RADICAL; 1. Complete proteome.
KW Oxidoreductase; Organic radical; FREE RADICAL (BY SIMILARITY).
FT MOD_RES 682 682 FREE RADICAL (BY SIMILARITY).
SQ SEQUENCE 707 AA; 80233 MW; A3795F7921A6781D CRC64;

Query Match      79.1%; Score 34; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EEDFYR 7
      |||||
Db     425 EEDFYR 430

Search completed: June 9, 2004, 15:49:06
Job time : 6.10811 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 23.4595 seconds
(without alignments)
94.147 Million cell updates/sec

Title: US-09-660-302D-7
Perfect score: 43
Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTEMBL_25.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	88.4	153	16 Q8R8G6	Q8R8G6 thermoanaer
2	38	88.4	632	6 Q95ML5	Q95ML5 salmirei bol
3	38	88.4	538	6 Q9XSZ1	Q9XSZ1 papio anubi
4	37	86.0	399	11 Q8VCQ7	Q8VCQ7 mus musculus
5	37	86.0	399	11 Q8C356	Q8C356 mus musculus
6	36	83.7	76	5 Q9U9B1	Q9U9B1 ancylostoma
7	36	83.7	91	5 Q16938	Q16938 ancylostoma
8	36	83.7	125	13 Q98SF6	Q98SF6 xenopus lae
9	36	83.7	206	4 Q14897	Q14897 homo sapien
10	36	83.7	325	13 Q98SF7	Q98SF7 xenopus lae
11	36	83.7	325	11 Q811Z4	Q811Z4 rattus norv
12	36	83.7	369	6 Q865X9	Q865X9 sus scrofa
13	36	83.7	378	13 Q90881	Q90881 gallus gall
14	36	83.7	388	11 Q80W90	Q80W90 rattus norv
15	36	83.7	397	4 Q86UH2	Q86UH2 homo sapien
16	36	83.7	400	13 O42108	O42108 gallus gall

17	36	83.7	726	10 Q9M9Y2	Q9M9Y2 arabidopsis
18	35	81.4	202	16 Q9PMX2	Q9PMX2 campylobact
19	35	81.4	219	10 Q8S056	Q8S056 oryza sativ
20	35	81.4	552	16 Q8ZQE6	Q8ZQE6 salmonella
21	35	81.4	552	16 Q8Z827	Q8Z827 salmonella
22	35	81.4	1376	5 Q26637	Q26637 strongyloce
23	35	81.4	1823	5 Q26638	Q26638 paracentrot
24	35	81.4	3198	5 Q26639	Q26639 strongyloce
25	34	79.1	102	16 Q8DZ48	Q8DZ48 streptococc
26	34	79.1	179	12 Q8JRV2	Q8JRV2 phthorinaea
27	34	79.1	182	5 Q8ISK6	Q8ISK6 plasmodium
28	34	79.1	262	5 Q8SU06	Q8SU06 encephalito
29	34	79.1	277	10 Q9SK11	Q9SK11 arabidopsis
30	34	79.1	331	16 Q97ID4	Q97ID4 clostridium
31	34	79.1	420	16 Q8RA45	Q8RA45 thermoanaer
32	34	79.1	457	16 Q7ML30	Q7ML30 bordetella
33	34	79.1	457	16 Q7W7P2	Q7W7P2 bordetella
34	34	79.1	457	16 Q7VV94	Q7VV94 bordetella
35	34	79.1	563	16 Q8YN67	Q8YN67 anabaena sp
36	34	79.1	592	11 Q64571	Q64571 rattus norv
37	34	79.1	599	11 Q922R3	Q922R3 mus musculu
38	34	79.1	625	3 Q94300	Q94300 schizosacch
39	34	79.1	1007	12 Q9QH62	Q9QH62 gallid herp
40	34	79.1	1256	5 Q8I575	Q8I575 plasmodium
41	34	79.1	1446	5 Q8IDQ5	Q8IDQ5 plasmodium
42	34	79.1	1595	4 Q8IVG6	Q8IVG6 homo sapien
43	33	76.7	98	5 Q16939	Q16939 ancylostoma
44	33	76.7	141	16 Q8DF30	Q8DF30 vibrio vuln
45	33	76.7	159	5 Q9W4Q9	Q9W4Q9 drosophila

ALIGNMENTS

RESULT 1

Q8R8G6 ID Q8R8G6 PRELIMINARY; PRT; 153 AA.
AC Q8R8G6
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein TTE2033.
GN TTE2033.
OS Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
RA "A complete sequence of T. tengcongensis genome."
RL Genome Res. 12:689-700(2002).
DR EMBL; AB013153; AAM25210.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 153 AA; 18428 MW; 3B0F4ED430B1A0FA CRC64;

Query Match 88.4%; Score 38; DB 16; Length 153;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6

Db 21 CEEDFY 26

RESULT 2

Q95ML5 ID Q95ML5 PRELIMINARY; PRT; 632 AA.
AC Q95ML5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

RESULT 4

O8VCQ7 PRELIMINARY; PRT; 399 AA.

ID Q8VCQ7

AC Q8VCQ7

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Open reading frame 6.

DE ORF6.

GN Mus musculus (Mouse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR MBL; BC019440; AAH19440.1; -.

DR MGD; MGI:1352481; ORF6.

DR InterPro: IPR007529; Znf_HIT.

DR Pfam; PF04438; zf-HIT; 1.

SQ SEQUENCE 399 AA; 42995 MW; B5CA88342B56932B CRC64;

Query Match 86.0%; Score 37; DB 11; Length 399;

Best Local Similarity 85.7%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEDDFYR 7

Db 41 CAEDFYR 47

RESULT 5

Q8C356 PRELIMINARY; PRT; 399 AA.

ID Q8C356

AC Q8C356

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN ORF6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Lung;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

DR EMBL; AK086863; BAC39755.1; -.

DR MGD; MGI:1352481; ORF6.

DR InterPro: IPR007529; Znf_HIT.

DR Pfam; PF04438; zf-HIT; 1.

KW Hypothetical protein.

SQ SEQUENCE 399 AA; 42896 MW; F4CF854CSB5FEC87 CRC64;

Query Match 86.0%; Score 37; DB 11; Length 399;

Best Local Similarity 85.7%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

RESULT 3

Q9XSZ1 PRELIMINARY; PRT; 638 AA.

ID Q9XSZ1

AC Q9XSZ1

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Growth hormone receptor.

OS Papio anubis (Olive baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Papio.

OX NCBI_TaxID=9555;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=99367319; PubMed=10425448;

RA Zogopoulos G., Nathanielsz P., Hendy G.N., Goodyer C.G.;

RT "The baboon: a model for the study of primate growth hormone receptor

gene expression during development.";

RL J. Mol. Endocrinol. 23:67-75 (1999).

DR EMBL; AF150751; AAD39536.1; -.

DR HSSP; P10912; 1AXI.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro: IPR002996; CRIA.

DR InterPro: IPR003961; FN.III.

DR InterPro: IPR003528; Hemtopoptn_L_F1.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor.

SQ SEQUENCE 632 AA; 70883 MW; 440E17AF6277EDA3 CRC64;

Query Match 88.4%; Score 38; DB 6; Length 632;

Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

Db 259 CEDDFY 264

us-09-660-302d-7.rspt

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDDFY 6

```

QY 1 CEEDFYR 7
Db 41 CAEDFYR 47

RESULT 6
Q9U9B1 PRELIMINARY; PRT; 76 AA.
AC Q9U9B1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ascaris type serine protease inhibitor (fragment).
OS Ancylostoma ceylanicum.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=53326;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison L.M., Cappello M.;
RT "The molecular cloning of an ascaris type serine protease inhibitor
RT from adult Ancylostoma ceylanicum hookworms.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172653; AAD51336.1; -.
DR HSP; P56682; 1CV.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01826; TIL; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Protease.
FT NON TER 1
SQ SEQUENCE 76 AA; 8385 MW; D35FCEF7C2088A53 CRC64;

Query Match 83.7%; Score 36; DB 5; Length 76;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 44 CEEGFYR 50

RESULT 7
Q16938 PRELIMINARY; PRT; 91 AA.
AC Q16938
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Anti-coagulant protein C2 precursor (fragment).
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98298519; PubMed=8700900;
RA Jaspers L.S., Messens J.H., De Keyser A., Eeckhout D.,
RA van den Brande I., Ganssems Y.G., Lauwereys M.J., Vlaek G.P.,
RA Staussens P.E.;
RT "Surface expression and ligand-based selection of cDNAs fused to
RT filamentous phage gene VI.";
RL Biotechnology 13:378-382(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312655; PubMed=8700900;
RA Staussens P., Bergum P.W., Ganssems Y., Jaspers L., Laroche Y.,
RA Huang S., Maki S., Messens J., Lauwereys M., Cappello M., Hotez P.J.,
RA Lasters I., Vlaek G.P.;
RT "Anticoagulant repertoire of the hookworm Ancylostoma caninum.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).
DR EMBL; U30793; AAC47080.1; -.

```

```

DR PDB; 1COU; 13-OCT-99.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF01826; TIL; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Signal.
FT NON TER 1
FT SIGNAL <1 7
FT CHAIN 8 91
FT CHAIN 8 91
SQ SEQUENCE 91 AA; 10358 MW; ECB11CB4597C24DA CRC64;

Query Match 83.7%; Score 36; DB 5; Length 91;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 59 CEEGFYR 65

RESULT 8
Q98SF6 PRELIMINARY; PRT; 125 AA.
AC Q98SF6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lhx2 protein (fragment).
GN LHX2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RA Bachy I., Vernier P., Retaux S.;
RT "The LIM-homeodomain family in the developing xenopus brain:
RT conservation and divergences with the mouse related to the evolution
RT of the forebrain.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
DR EMBL; AJ311712; CAC35215.1; -.
DR HSP; P32965; 1CTL.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN 1; 1.
DR PROSITE; PS00023; LIM_DOMAIN 2; 2.
KW LIM domain; Metal-binding; Zinc.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 14283 MW; 375E42A29104D364 CRC64;

Query Match 83.7%; Score 36; DB 13; Length 125;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 28 CKEDFYR 34

RESULT 9
Q14897 PRELIMINARY; PRT; 206 AA.
AC Q14897
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

DE L-myc protein (similar to lung carcinoma myc related oncogene 1).
GN L-MYC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=88094386; PubMed=2827002;
RA Kaye F., Battey J., Nau M., Brooks B., Seifter E., De Greve J.,
RA Birrer P., Sausville E., Minna J.;
RT "Structure and expression of the human L-myc gene reveal a complex
RT pattern of alternative mRNA processing.";
RL Mol. Cell. Biol. 8:186-195(1988).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; M19720; AAA59878.1; -;
DR EMBL; BC011864; AAH11864.1; -;
DR TRANSFAC; T02386; -;
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003700; F:transcription factor activity; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro; IPR002418; TF MYC.
DR Pfam; PF01056; MYC N term; 1.
DR PRINTS; PR00044; LEUZIPRMVC.
DR SEQUENCE 206 AA; 21766 MW; 595C9CD6C9A8EC71 CRC64;
SQ
Query Match 83.7%; Score 36; DB 4; Length 206;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CEEDFYR 7
DB 15 CGEDFYR 21
RESULT 10
Q98SF7 PRELIMINARY; PRT; 217 AA.
AC Q98SF7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lhx9 protein (Fragment).
GN LHX9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipioidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Head;
RC Bachy I., Vernier P., Retaux S.;
RA "The LIM-homeodomain family in the developing xenopus brain:
RT conservation and divergences with the mouse related to the evolution
RT of the forebrain.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
DR EMBL; AJ311711; CAC35214.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.

DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
DR PROSITE; PS00478; LIM DOMAIN_1; 1.
DR PROSITE; PS00023; LIM DOMAIN_2; 1.
DR LIM domain; Metal-binding; Zinc.
FT NON_TER 1
FT NON_TER 217
SQ SEQUENCE 217 AA; 24716 MW; 6CBB88B595ECB851 CRC64;
Query Match 83.7%; Score 36; DB 13; Length 217;
Best Local Similarity 71.4%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEEDFYR 7
DB 27 CKEDYR 33
RESULT 11
Q811Z4 PRELIMINARY; PRT; 325 AA.
ID Q811Z4
AC Q811Z4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LIM-homeodomain type transcription factor Lhx9 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Wistar;
RA Mazaud S., Oreal E., Guigon C.J., Carre-Busebe D., Magre S.;
RT "Lhx9 expression during gonadal morphogenesis as related to the state
RT of cell differentiation.";
RL Gene Expr. Patterns 2:373-377(2002).
DR EMBL; AF527619; AAO27570.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
DR PROSITE; PS00478; LIM DOMAIN_1; 2.
DR PROSITE; PS00023; LIM DOMAIN_2; 2.
DR Homeobox; DNA-binding; Nuclear protein.
FT NON_TER 1
FT NON_TER 325
SQ SEQUENCE 325 AA; 36429 MW; CCA307A920FAB8AB CRC64;
Query Match 83.7%; Score 36; DB 11; Length 325;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEEDFYR 7
DB 89 CKEDYR 95
RESULT 12
Q865X9 PRELIMINARY; PRT; 369 AA.
ID Q865X9

AC Q845X9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LIM-homeobox protein 9 (Fragment).
 OS Sus scrofa (Fig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Paradis V.R., Forget C.L., Silversides D.W.;
 RT "Sus scrofa Lhx9 mRNA";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY240953; AA085392.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 KW DNA-binding; Homeobox; LIM domain; Nuclear protein.
 FT NON TER 369 369
 SQ SEQUENCE 369 AA; 41025 MW; 9C8FA3ADF572F9AE CRC64;
 Query Match 83.7%; Score 36; DB 6; Length 369;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CEEDFYR 7
 DB 120 CKEDYR 126
 RESULT 13
 Q90881
 ID Q90881 PRELIMINARY; PRT; 378 AA.
 AC Q90881;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Homeobox protein.
 DE LH-2
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Trembl G., Jessell T.M.;
 RT "Differentiation of dorsal commissural neurons defined by expression of the LIM homeobox gene LH-2: Suppression by notochord grafts and maintained after notochord removal";
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC IONS.
 DR EMBL; L35566; AA50258.1; -;
 DR PIR; JC5658; JC5658.
 DR HSP; P32965; ICTL.
 DR GO; GO:0005634; C:nucleus; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein; Zinc.
 SQ SEQUENCE 378 AA; 42007 MW; 34220850FCB82FFC CRC64;

Query Match 83.7%; Score 36; DB 13; Length 378;
 Best Local Similarity 71.4%; Pred. No. 48;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 DB 101 CKEDYR 107

RESULT 14
 Q80W90
 ID Q80W90 PRELIMINARY; PRT; 388 AA.
 AC Q80W90;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LIM-homeobox type transcription factor Lhx9.
 DE Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shan Y.X., Pan J., Geng D.C., Gu M.Y., Yu L.;
 RT "Cloning and characterization of Rat Lim-homeobox domain type transcription factor Lhx9";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY273890; AAP32472.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR InterPro; IPR007107; LIM homeo.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 388 AA; 42934 MW; EFB0ESB612A3729C CRC64;

Query Match 83.7%; Score 36; DB 11; Length 388;
 Best Local Similarity 71.4%; Pred. No. 49;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
 DB 111 CKEDYR 117

Thu Jun 10 08:23:55 2004

```

RESULT 15
Q86UH2
ID Q86UH2 PRELIMINARY; PRT; 397 AA.
AC Q86UH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LIM-homeobox 9 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shan Y.X., Pan J., Guo Z.K., Geng D.C., Huang C.Q., Yu L.;
RT "Cloning and characterization of human novel LIM-homeobox 9 gene."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY273889; AAP32471.2; -.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 397 AA; 43976 MW; FA8BBB550A5FCE03 CRC64;

Query Match 83.7%; Score 36; DB 4; Length 397;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFYR 7
Db 120 CKEDYR 126

```

Search completed: June 9, 2004, 15:51:24
Job time : 25.4595 secs